	Copyright	GenCore (c) 1993	GenCore version 5.1.6 c) 1993 - 2005 Compuç	GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	
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Run on:	September 8	, 2005,	22:23:54 (v 16	<pre>September 8, 2005, 22:23:54 ; Search time 738.572 Seconds (without alignments) 16735.564 Million cell updates/sec</pre>	

1 gaccttaaatatatcgaggt.....tactacaaacacctctacgc 2088 US-09-974-546C-83 2088 Title: Perfect score: Scoring table: Sequence:

4390206 segs, 2959870667 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched:

8780412 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AAZ87583 AAS04000 AAZ87584 AAS04001 AAV16883 AAX26018 AAZ87503 AAS03722 ü Score 2076 Result

Human pro Prostate Biomarker Human col DNA encod Human ova Human ova Aaz87583 Prostate Aas04000 Biomarker Biomarker Prostate, DNA encod Prostate DNA DNA DNA DNA DNA Description Aax26018 Aaz87503 Aas1322 Aas1722 Aas7936 Abt77086 Abs71702 Aas71702 Aas7271 Aas7336 Aas7336 Aas73736 Aas73736 Aas81380 Aas72059 Aas71116 Aaz87584 Aas04001 Aav16883 AAA16415 AAS79336 ABT07086 ABX72964 AAS75366 AAS79702 AAS81380 AAS72059 AAS71116 AAS92271 % Query Match Length DB 1167 1167 1167 1167 1167 1205 1205 430 115.2 115.2 115.2 115.2 1950 275.4 275.4 275.4 1115.6 1115.6 115. 115. 115. 115 υυ 000

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AAS71114	AAS72053	AAS71240	AAS70932	AAS91719	AAS69594	AAS73101	AAS83831	AAS64322	AAS85521	AAS81821	AAS73106	AAS74903	AAS78969	AAS71603	AAS73165	AAS77246	AAS71650	AAS76929	AAS72643	AAS76709	AAS66493	AAS78788	AAS71125	AAS92377
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ALIGNMENTS

BP AAZ87583 standard; DNA; 2088

AAZ87583;

(first entry) 19-APR-2000

Prostate disease marker UC Band #28

Nucleic acid marker; biomarker; tumour; prostate cancer; bladder cancer; benign prostatic hyperplasia; BPH; breast cancer; human; immunodetection; diagnosis; PCR primer; ss.

Homo sapiens.

WO9964631-A1

16-DEC-1999

99WO-US013151 11-JUN-1999; 98US-00097199 12-JUN-1998;

(UROC-) UROCOR INC

Veltri RW; Ralph D, O'hara SM, An G,

WPI; 2000-116557/10. P-PSDB; AAY59295 Novel RNA biomarkers for diagnosis, prognosis and management of prostate, breast and bladder cancer.

Claim 1; Page 182-183; 191pp; English.

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The invention provides nucleic acid markers of prostate, breast and bladder cancer. The markers are indicators of malignant transformation of prostate, breast and bladder tissues and are diagnostic of the potential for metastatic spread of malignant prostate tumours. The nucleic acid can also be used as targets for therapeutic intervention in prostate cancer, benign prostatic hyperplasia (BPH), bladder cancer or breast cancer. The markers may be used to design specific probes and primers, for the rapid AAZ87583

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complysis of prostate, bladder or breast biopsy samples. The probes and prime may also be used for in situ hybridization or in situ PCR detection and diagnosis. They may also be used to identify and isolate control of the polypeptide products of the markers can be used to treat prostate control of the polypeptide products of the markers can be used to treat prostate control of the polypeptide products of the markers can be used to treat prostate control of the proteins and antibodies can be used in immunodetection methods for detecting or quantifying the cancers, and for clinical diagnosis of these cancers. The antibodies may also be used for calinical diagnosis of these cancers. The encoded proteins XX Sequence 2088 BP; 740 A; 406 C; 337 G; 604 T; 0 U; 1 Other;	Query Match 100.0%; Score 2087.6; DB 3; Length 2088; Best Local Similarity 100.0%; Pred. No. 0; Matches 2088; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 1 GACCTTAAATATATCAAGTGGCTAATTGATCTATAATAATATTACAAAATTATCTTCTA 60 Db 1 GACCTTAAATATCGAGGTGGCTAATTGATGTATAATAATATACAAATTTACAAATTTCTTCTA 60	Qy 61 TTGCTACAGAGCTACAATTTACAGTAGGCCACCATGAGGGCCTTCTTAAGGAACC 1.20 Db 61 TTGCTACAGAGCTACAATTCAATTTACAGTAGGCCACCATGAGGGCCTTCTTAAGGAACC 1.20	Oy 121 AGAATATGAGGATATGCACAATATTATTCACATTTTACAGATCAGAAATTGAGGCACA 180 	OY 181 GATTAAGTAACTTCCCAAGGCTACCAGGCATTCTAGCTCCAGAAACTGTGCTCTTACCAT 240	OY 241 TCTGCTACAAGGTATTTCGAAAAAAAAAAAAAGTAAAAGGAAGG	OY 301 TCATTGATTATTCCATAGAACAGTCACACGCATGCAATTCTCACACCCTTGCAGACACACT 360 Bb 301 TCATTGATTATTCCATAGAACAGTCACATGCAATTCTCACACTTGCAGACACACT 360	Qy 361 TGACCATGAAAGGTTCCTCAATGAAATGTTCCTCATTATCTTCAGAAGCCATATTATTCA 420 	Qy 421 CATTGACTTTGCAGTTAACTCAGACCCTAGGTCTGGAATGCTGTCTTCTTCTATCCA 480	Qy 481 AAACTATACATCCACAGATCATATAAACTCTCAGCCCTGCAGAAGCCTTTCCAGAAAA 540 	Qy 541 ATAAAATGGTTGAAAAGGCAATTCTGCTACCAATGACTGTTTAAGCCCAGCCAAGTAAC 600 Db 541 ATAAAAATGGTTGAAAAGGCAATTCTGCTACCAATGACTGTTTAAGCCCAGCCAAGTAAC 600	601	Oy 661 AATTCTAAAATACAAACCCATGTTGATCTTTCTCAATCTTGAACTCATAGATTATTATCT 720	721 ATTRACTORALTETTACTORALTETTACTORACTORACTORACTORALTETTACTORACTORALTETTT	721 ATTATCTCAATTTAGTTTGTTATTTATCCTAGTGGGCCATTAAAAACTACCACATGTTT	781 TCTGTCTCTCCATTAGTCAATAACTAAACGAGCAATTAGTAAGCCATGTGCCAGAT	DD 781 TCTGTCTCCATTAGTCAATAACTAAGGAGGAATTAGTAAGCCATGTGCCAGAT 840
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l è	1621	TITIBGACACTITICCONGCANTAACTIGCACAAACAATTATIGGAACAAACTITIGTITIBGATICAACTI
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ò	1691	CTCCAACAACGACACATTCAGGAGTTAAATATTTTTCATCAAACATTGGATTTTTCCTTA 1740
qq	1681	CTCCAACAACGACACATTCAGGAGTTAAATATTTTCATCAAACATTGGATTTTTCCTTA 1740
λõ	1741	ACGCTAGAGATTGCTACAAATCTTCTGAAGGGTCTCCAATGGCTTCAGGCTAAGAAGAGAT 1800
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à i	1801	TTCTCCCTGTTATAAGCAGCAGAAATTAGCCATTTCACTCTCAAACTTCACTAATGA 1860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acids as biomarkers and targets useful for detecting, diagnosing, prognosing, and in developing treatments for prostate, breast and bladder cancer.
1981 AAGAGAGAAGAATCAAATAGACACAATAAAAATGATAAAGGGGATATCACCACCGATCC
                                                                        AAGAGAGAAGAATCAAATAGACACAATAAAAAATGATAAAGGGGATATCACCACCGATCC
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                                                                                                                                                                                         2041 CACAGAAATACAAACTACCATCAGAGAATACTACAAACACCTCTACGC 2088
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96US-00692787.
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P-PSDB; AAU02174.
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Best Local Similarity
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11-JAN-1996;
31-JUL-1996;
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Key

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AAS04000 RESULT

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Prostate disease marker UC Band #28 splice variant.

(first entry)

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RESULT 3 AAZ87584 ID AAZ87584 standard; DNA; 2506

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The invention provides nucleic acid markers of prostate, breast and bladder cancer. The markers are indicators of malignant transformation of prostate, breast and bladder tissues and are diagnostic of the potential for metastatic spread of malignant prostate tumours. The nucleic acid can also be used as targets for therapeutic intervention in prostate cancer. The benign prostatic hyperplasia (BPH), bladder cancer or breast cancer. The markers may be used to design specific probes and primers, for the rapid or primers may also be used for in situ hybridization or in situ PCR detection and diagnosis. They may also be used to identify and isolate the polypeptide products of the markers can be used to treat probes and to plypeptide products of the markers can be used to treat prostate cancer. bladder cancer or breast cancer. The encoded protains may be used to detect antibodies. The proteins and antibodies can be used in immunodetection methods for detecting or quantifying the cancers, and for climical diagnosis of these cancers. The encoded proteins may also be used for radioimaging to quantify and localize the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel RNA biomarkers for diagnosis, prognosis and management of prostate,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  O'hara SM, Ralph D, Veltri RW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 184-186; 191pp; English.
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Best Local Similarity 99.5
Matches 1968; Conservative
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	AASO4001 standard; CDNA; 2505 BP. AASO4001; 29-AUG-2001 (first entry) Blomarker UC band 28 #3, used in diagnosis and prognosis of cancer. Prostate; breast; bladder; cancer; biomarker; probe; diagnostic; benign prostatic hyperplasia; BPH; therapeutic; human; ss. Homo sapiens. Key 99506 /*tag= a /product= "Prostate cancer marker protein" US6218529-B1. 17-APR-2001. 12-JUN-1998; 98US-000097199. 31-JUL-1995; 95US-0013615P. 31-JUL-1995; 96US-0013611P.
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New nucleic acids as biomarkers and targets useful for detecting, diagnosing, prognosing, and in developing treatments for prostate, breast and bladder cancer.
                                                                                                                   sequence represents nucleic acid biomarker UC band 28 #3, used in
                                                                                                   Claim 2; Col 121-125; 78pp; English
                        Ralph D,
                                        WPI; 2001-289849/30
P-PSDB; AAU02175.
        (UROC-) UROCOR INC
                        O'hara SM,
                        An G,
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detection of prostate, breast and bladder cancer. Biomarker incleic acid sequences can be used as hybridisation probes and primers that specifically hybridise to prostate cancer. benign prostatic hyperplasia (BPH), bladder cancer or breast cancer markers. Proteins encoded by the nucleic acid markers can be used to produce antibodies for the detection of prostate, breast or bladder cancer. The nucleic acids can be used as targets for therapeutic intervention in these diseases, in the identification and isolation of full-length gene sequences, including regulatory elements for gene expression, from genomic human DNA libraries as hybridisation probes for screening genomic human DNA libraries. The kits comprising the nucleic acid sequences are useful for detecting bladder, breast or prostate cancer cells in a biological sample

Seguence 2505 BP; 822 A; 519 C; 446 G; 718 T; 0 U; 0 Other;

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දු දු	661	661 AATTCTAAATACAAACCCATGTTGATCTTTCTCAATCTTGAACTCATACATTATTTT 720
È	721	ATTATCTCAATTTAGTTTGTTATCTAGTGGGCCATTAAAACTACCACATGTGTT 780
QQ	721	ATTATCTCAATTTAGTTTGTTATTTATCCTAGTGGGCCATTAAAAACTACCACATGTGTT 780
à	781	TCTGTCTCTCCATTAGTCAATAACTAAACTAACGAGCAATTAGTAAGCCATGTGCCAGAT 840
ΩD	781	TCTGTCTCTCCATTAGTCAATAACTAAAGGAGCAATTAGTAAGCCATGTGCCAGAT 840
ò	841	GCTCCGCTAGGCACCAGAGGATAAAAACAATACTTATAGTATACCACTAATTTTCGCTT 900
QQ	841	GCTCCGCTAGGCACCAGAGGATAAAAACAATACTTATAGTATACCACTAATTTTCGCTT 900
ò	901	AGTAACTAGTGAAATGTTCAAGTCATGCCTGAGTGCAGAGGTTGAGGAGACATTACAATGT 960
QQ	901	AGTAACTAGTGAAATGTTCAAGTCATGCCTGAGTCAAGAGTTGAGGAGACATTACAATGT 960
ò	961	
Ор	961	
ò	1021	TAATIGATITCIGACICIAICATIGGCCTCCAAACACAGAIIGIGITITICITIGGITIT 1080
Ор	1021	
Š	1081	
Db	1081	GTTTTCTTCACTATGGGATCTTCTGTGCCCAGCACAGTGCCTGACATAGAAAACAATC 1140
δ	1141	AATATTTGCTGAATAAATGATTAAAAAATCAGAGAACTTTCCCATTCTGTTTGGATCTAT 1200
ΟP	1141	AATATTTGCTGAATAAATGATTAAAAAATCAGAGAACTTTCCCATTCTGTTTGGATCTAT 1200
ò	1201	
qq	1201	
٥'n	1261	
Ωp	1261	
È	1321	TGGTGGTGCTTTAAAAAGATATTAATAGATAATATGAAAATCTCCATCTCAAAAATAATG 1380
QQ	1321	
ò	1381	
QQ	1381	
δ	1441	CATATATITITACCATCTGCAAGGCAGTCATATCAAAGGGTAAAGAAAGA
Ор	1441	CATATATTTTTACCATCTGCTGAAGGCAGTCATATCAAAGGCTAAAGAAAG
ò	1501	AAACTCAGTAAGAATTATATTAGTCTGTTTGCAAAGTAGAAAAAGATTCTCATCACTCAA 1560
qa	1501	
ઠે	1561	
qq	1561	CCTTATGAGCAGGAAGAGGGAAGGCTGTTTGAGAACCATTTACTTAGCAGAACCACATAT 1620
ò	1621	TITAGACACTICCCTGCATTAACTGCACAAACAATAIGITTGCAAACTIGITKGAICAAC 1680
OP OP	1621	TTTAGACACTTCCCTGCATTAACTGCACAAACAATATGTTTGCAAACTTGTT-GATCAAC 1679

1805

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1746 AGAGATTGCTACAAATCTTCTGAAGGGTCTCAATGGCTTCAGGCTAAGAAGAGATTTCTC

1686 ACAACGACATTCAGGAGTTAAATATTTTTCATCAAACATTGGATTTTTCCTTAACGCT 1 ACAACGACACATTCAGGAGTTAAATATTTTTCATCAACATTGGATTTTTTCCTTAACGCT

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Gaps

; 0 757;

11; DB 2;

Score 275.4; DB 2 Pred. No. 9.3e-53;); Mismatches 11

13.2%; 96.2%;

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Matches 282; Conservative

Similarity

Query Match Best Local (

Length Indels 1865

1866 TTCTTTCCAAAAGGAACTCTAGAAGACCAAATGCCCCGAGTTAAGAACATCAAAACTAAC 1925

181 TICTTTCCAAAAGGAACTCTAGAAGACCAAATGCCCCGAGTTAAGAACATCAAAACTAAC

CATCTGAAGAAACTTCCCAAGTGTAAGACTCTGCCTGCACGACAACACATAAA 1978 CATCTGAAGAACTTCCCAAGTGTAAGACTCTGCCATTAAAACATTACCGAGA 293

1926

241

121 CCTGTTATAAGCAGCAAGACAAATTAGCCATTTCACTCTCAAACTTCACTAATGATCACA

CCTGTTATAAGCAGCAAGACAAATTAGCCATTTCACTCTCAAACTTCACTAATGATCACA

240

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This represents a marker sequence for human prostate cancer. Isolated nucleic acid segments shown in AAV16881 to AAV16885, AAV16890 to AAV16803, AAV26351 and AAV26352 which can act as human prostate cancer markers are provided in the specification. It also provides methods for identifying markers for human prostate cancer and for detection of prostate cancer cells. The markers can be identified by amplifying human prostate cancer and for detection of prostate cancer cells. The markers can be identified by amplifying human prostate cancer want are differentially expressed the products and identifying those RNA that are differentially expressed the products and identifying those RNA that are differentially expressed between human prostate cancers versus normal or benign human prostate. The nucleic acid being a prostate cancer marker. The nucleic acid being a prostate cancer marker. Primers and probes derived from this marker can be used for the detection of prostate cancer cells in a sample. Antibodies against the protein and oligonucleotides antisense to the marker nucleic acid fragments, inhibitors of the protein and oligonucleotides antisense to the marker can be used for the antisense to the marker nucleic and fragments, inhibitors of the protein and oligonucleotides antisense to the marker can be used for the diagnosis of human prostate cancer. The antibodies can also be used for the diagnosis of human prostate cancer.
1800
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                                                                                                                                                            1860
                                                                                                                                                                                               1800 Tricriccitarranaccaccaacaaarraccarriccacriccaaacricacraarga 1859
                                                                                                                                                                                                                                      1861 TCACATTCTTTCCAAAAGGAACTCTAGAAGACCCAAATGCCCCGAGTTAAGAACATCAAAA 1920
                                                                                                                                                                                                                                                              1860 TCACATTCTTTCCAAAAGGAACTCTAGAAGACCAAATGCCCCGGGTTAAGAACATCAAAA 1919
                                                                                                                                                                                                                                                                                                                   1920 CTAACCATCTGAAGAAACTTCCCAAGTGTAAGACTCTGCCATTAAAACATTACCGAGA 1977
                                                                               ACGCTAGAGATTGCTACAAATCTTCTGAAGGGTCTCAATGGCTTCAGGCTAAGAAGAGT
                                                                                                                  1740 ACGCTAGAGATTGCTACAAATCTTCTGAAGGGTCTCAATGGCTTCAGGCTAAGAAGAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human prostate cancer marker – useful for detection and treatment of human prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prostate cancer; human; marker; diagnosis; treatment; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Band #28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 133-134; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ralph D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human prostate cancer marker UC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV16883 standard; DNA; 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UROC-) UROCOR INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Veltri R,
                                                                                                                                                          1801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV16883;
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The invention relates to methods for diagnosing prostate cancer or benign prostatic hyperplasia cells in a biological sample. The method uses digonucleotide probes specific for marker genes associated with tumour differentiation and progression in Reverse Transcription Polymerase Chain Reaction (RT-PCR) analysis. The methods are diagnostic techniques useful for detecting and monitoring the progression of benign prostatic and human prostate cancer (the most prevalent form of cancer and a major cause of death in males) prior to the tumor undergoing metastasis, therefore allowing the optimal method of treatment to be determined before the condition becomes life threatening. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diagnosing prostate cancer and benign prostatic hyperplasia cells - using oligonucleotide probes specific for marker genes associated with tumor differentiation and progression in Reverse Transcription Polymerase Chain
                                                                                                                                                                           Prostate cancer; benign prostatic hyperplasia; marker gene; tumou; differentiation; Reverse Transcription Polymerase Chain Reaction; diagnostic; progression; cancer; metastasis; human; RT-PCR; ss.
                                                                                                                                             Prostate disease marker gene fragment UC Band #28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O'hara SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Col 71-72; 74pp; English.
                                     ВР
                                                                                                                                                                                                                                                                                                                                                                 96US-00692787.
                                                                                                                                                                                                                                                                                                                                                                                                   95US-0001655P
                                   AAX26018 standard; DNA; 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An G,
                                                                                                         20-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Veltri R, Ralph D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-214055/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (UROC-) UROCOR INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reaction analysis.
                                                                                                                                                                                                                                                                                                                                                                 31-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                     31-JUL-1995;
                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                           US5882864-A
                                                                                                                                                                                                                                                                                                                               16-MAR-1999
                                                                     AAX26018;
RESULT 6
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Sequence 757 BP; 228 A; 190 C; 147 G; 192 T; 0 U; 0 Other;

us-09-974-546c-83.rng

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full length gene sequences form various DNA libraries. Antibodies against the polypeptide products of the markers can be used to treat prostate cancer, bladder cancer or breast cancer. The encoded proteins may be used to detect antibodies. The proteins and antibodies can be used in immunodetection methods for detecting or quantifying the cancers, and for clinical diagnosis of these cancers. The antibodies may also be used for radioimaging to quantify and localize the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acids as biomarkers and targets useful for detecting, diagnosing, prognosing, and in developing treatments for prostate, breast and bladder cancer.
     detection and diagnosis. They may also be used to identify and isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1806 CCTGTTATAAGCAGCAAGACAAATTAGCCATTTCACTCCCAAACTTCACTAATGATCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1866 TTCTTTCCAAAAGGAACTCTAGAAGACCAAATGCCCCGAGTTAAGAACATCAAAACTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 TTCTTTCCAAAAGGAACTCTAGAAGACCAAATGCCCCGAGTTAAGAACATCAAAACTAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CCTGTTATAAGCAGCAAGACAAATTAGCCATTTCACTCTCAAACTTCACTAATGATCACA
                                                                                                                                                                                                                                                                                                                                                                                                                      1 ACAACGACACATTCAGGAGTTAAATATTTATCATCAAACATTGGATTTTTCCTTAACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AGAGATTGCTACAAAATCTTCTGAAGGGTCTCAATGGCTTCAGGCTTAGAAGAAGAGATTTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biomarker UC band 28 #1, used in diagnosis and prognosis of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATCTGAAGAAACTTCCCAAGTGTAAGACTCTGCCATTAAAACATTACCGAGA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prostate; breast; bladder; cancer; biomarker; probe; diagnostic; benign prostatic hyperplasia; BPH; therapeutic; human; 88.
                                                                                                                                                                                                                                                                    13.2%; Score 275.4; DB 3; Length 757; 96.2%; Pred. No. 9.3e-53; artive 0; Mismatches 11; Indels 0
                                                                                                                                                                                                                         Sequence 757 BP; 228 A; 190 C; 147 G; 192 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Veltri R;
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96US-0013611P.
96US-00692787.
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                                                                                                                                                                                                                                                                                                                         Matches 282; Conservative
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                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-1995;
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31-JUL-1996;
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                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid marker; biomarker; tumour; prostate cancer; bladder cancer; benign prostatic hyperplasia; BPH; breast cancer; human; immunodetection;
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                                                                                                                                                                                             1686 ACAACGACACATTCAGGAGTTAAATATTTTTCATCAAACATTGGATTTTTCCTTAACGCT
                                                                                                                                                                                                                              1 ACAACGACACTTCAGGGGTTAAATTTTATCATCAAACATTGGATTTTTCCTTAACGCT
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                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATCTGAAGAAACTTCCCAAGTGTAAGACTCTGCCTGCACGACAACACATAAA 1978
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                                                                                                  Length 757;
                                               Sequence 757 BP; 228 A; 190 C; 147 G; 192 T; 0 U; 0 Other;
                                                                                                                                               Indels
sequence represents a claimed marker gene fragment
                                                                                             Query Match 13.2%; Score 275.4; DB 2; Best Local Similarity 96.2%; Pred. No. 9.3e-53; Matches 282; Conservative 0; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ87503 standard; cDNA; 757 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        breast and bladder cancer.
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RESULT 7

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The sequence represents nucleic acid biomarker UC band 28 #1, used in detection of prostate, breast and bladder cancer. Biomarker nucleic acid sequences can be used as hybridisation probes and primers that specifically hybridise to prostate cancer, benign prostatic hyperplasia (BPH), bladder cancer or breast cancer markers. Proteins encoded by the nucleic acid markers can be used to produce antibodies for the detection of prostate, breast or bladder cancer. The nucleic acids can be used as targets for therapeutic intervention in these diseases, in the identification and isolation of full-length gene sequences, including regulatory elements for gene expression, from genomic human DNA libraries, as hybridisation probes for screening genomic human DNA libraries. The kits comprising the nucleic acid sequences are useful for detecting bladder, breast or prostate cancer cells in a biological sample
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 TTCTTTCCAAAAGGAACTCTAGAAGACCAAATGCCCCGAGTTAAGAACATCAAAACTAAC
                                                                                                                                                                                                                                                                                                                                                                             1686 ACAACGACACATTCAGGAGTTAAATATTTTCATCAAACATTGGATTTTTCCTTAACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1746 AGAGATTGCTACAAATCTTCTGAAGGGTCTCAATGGCTTCAGGCTAAGAAGAGATTTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AGAGATTGCTACAAATCTTCTGAAGGGTCTCAATGGCTTCAGGCTAAGAAGAGATTTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 CCTGTTATAAGCAGCAAGACAAATTAGCCATTTCACTCTCAAACTTCACTAATGATCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCTTTCCAAAAGGAACTCTAGAAGACCAAATGCCCCGAGTTAAGAACATCAAAACTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                1 ACAACGACACATTCAGGAGTTAAATATTTATCATCAAACATTGGATTTTTCCTTAACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human colon cancer differentially expressed nucleotide sequence #420.
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Steinmann KE, Astle JH, Burgess CC, Carroll E;
Dwivedi P, Ford DM, Lewis ME, Molino GA, Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1926 CATCTGAAGAAACTTCCCAAGTGTAAGACTCTGCCTGCACGACAACACATAAA 1978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Colon cancer, detect; differential expression; human; treatment; detect mutation; non-invasive diagnostic method; ds.
                                                                                                                                                                                                                                                                                                      DB 4; Length 757;
                                                                                                                                                                                                                                                                 Sequence 757 BP; 228 A; 190 C; 147 G; 192 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                        0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                    Score 275.4; DB 4 Pred. No. 9.3e-53;
                                                                                                                                                                                                                                                                                                    13.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA16415 standard; DNA; 573
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                                                                                                                                                                                                                                                                                                                     Best Local Similarity 96.2
Matches 282; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-256641/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FARB ) BAYER CORP.
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Catino TJ,
Schlegel R;
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                                                                                                                                                                                                                                                                                                      Query Match
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AAA16415/c
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                                                                                                                                                                      This sequence represents a human nucleotide sequence which is differentially expressed in colon cancer cells compared to the expression levels in normal calls. The nucleotide sequence can be used as a source of primers and probes. The nucleotide sequence is useful for determining the phenotype of a cell by detecting the differential expression of the sequence relative to a normal cell. The probes derived from the sequence an also be used to determine the phenotype of cells in a sample. Probes and antibodies which hybridise to the nucleotide sequence can also be used to determine the phenotype of a cell. The primers are useful for detecting a mutation in a test nucleotide sequence and also for detecting cancer, preferably colon cancer. Antiboddes against the protein encoded by the nucleotide sequence can also be used in a method to detect colon cancer. The diagnostic method is non-invasive and accurate for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2025 ATATCACCACCGATCCCACAGAAATACAAACTACCATCAGAGAATACTACAAACACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1965 CGACAACACATAAAAAAGAGAGAAAGAATCAAATAGACACAATAAAAATGATAAAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 ATATCACCACCGATCCCACAGAAATACAAACTACCATCAGAGAATACTACAAAACACCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Novel nucleic acids and proteins for identifying therapeutic agents useful for treating and diagnosing cancer, especially colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 573 BP; 98 A; 91 C; 111 G; 236 T; 0 U; 37 Other;
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                                                                                                             Claim 16; Page 294; 345pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS79336 standard; cDNA; 4051 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   colon cancer at an early stage
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23-AUG-2000; 2000US-00649167
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Best Local Similarity 95.2
Matches 118; Conservative
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P-PSDB; ABG15149.
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Mitcham JL,

Lodes MJ,

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Composition for detecting and treating ovarian cancer, comprises a specific polypeptide, polynucleotide, T cell population, or antigen
                                                                                                                                   Example 1; Page 94; 188pp; English.
                                              WPI; 2002-598720/64.
                                                                                                         presenting cell
                Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating of supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders polypeptide and polymucleotide sequences have applications in diagnostics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. Abs64197-A8645454 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed apecification, but was obtained in electronic format directly from MPO at the printed apecification, but was obtained in electronic format directly from MPO at the first sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1867 AAATGATAAAGGGGATATCACCACCGATCCCACAGAAATACAAACTACCATCAGAGAATA 1926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2011 AAATGATAAAGGGGATATCACCACCGATCCCACAGAAATACAAACTACCATCAGAGAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human ovarian cancer associated coding sequence SEQ ID NO: 248.
                                                                                                                                                                                                                                                                                                                                                                                                                DB 5; Length 4051;
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4051 BP; 1562 A; 824 C; 819 G; 846 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.5%; Score 115.6; DB 5; Length Best Local Similarity 89.9%; Pred. No. 4.3e-16; Matches 124; Conservative 0; Mismatches 14; Indels
                           Claim 1; SEQ ID NO 15140; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; ovarian cancer; cancer; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2071 CTACAACACCTCTACGC 2088
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99US-00246429.
99US-00397787.
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(LODE/) LODES M J.
(MITC/) MITCHAM J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KING G E.
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08-FEB-1999;
 biodiversity
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(MITC/)
(KING/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 CACCACGATCCCACAGAAATACAAACTACCATCAGAGAATACTACATACTACAAACACCTCTACGC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, cancer detection, ovarian carcinoma antigen, ovarian cancer, tumour antigen; tumour, OV2; OV3; OV6; OV9; OV10; OV12; OV14; OV17; OV18; OV23; OV24; OV27; OV41; OV54; OV57; gene; ss.
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                                                                                                                                                                               to treat cancer. The
The present invention relates to a method of detecting the presence of ovarian cancer in a patient, involving detecting ovarian cancer associated polynuclectides. The method is not only used to detect the presence of cancer, preferably ovarian cancer in a patient, but also is used to stimulate and/or expand T cells specific for an ovarian tumour protein. The sequences can be used in vaccines used to treat cancer. The present sequence is an ovarian cancer associated coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1969 AACACATAAAAAAGAGAGAGAAGAATCAAATAGACACAATAAAAAATGATAAAGGGGATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295 AATAAAGAAAAAAAAGAGAGAAGAATCAAATAGACACAATAAAAAATGATAAAGGGGGTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                       Query Match 5.5%; Score 115.2; DB 6; Length 430; Best Local Similarity 97.5%; Pred. No. 2.7e-16; Matches 117; Conservative 0; Mismatches 3; Indels 0
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                                                                                                                                                                                                                                                                              Sequence 430 BP; 70 A; 74 C; 85 G; 196 T; 0 U; 5 Other;
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ID ABX72964 standard; cDNA; 430
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08-FEB-1999;
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presence or absence of cancer in patient. The method comprising contacting a biological sample with an oligonucleotide that hybridises to partial polymucleotide sequence encoding for human ovarian carcinoma antigen, or its complement. The method and compositions are useful for the therapy and diagnosis of ovarian cancer. The method can be used to identify tumour antigens that are secreted from ovarian carcinoma and/or other tumours. Effective cancer detection is achieved using the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                     176
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                                                                                                                                           the invention. ABX72720-ABX73050 represent partial cDNA sequences encoding human ovarian carcinoma antigens
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                                                                                                                                                                                                                                               Score 115.2; DB 8; Length 430; Pred. No. 2.7e-16;
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                                                                                                                                                                                                      Sequence 430 BP; 70 A; 74 C; 85 G; 196 T; 0 U; 5 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding novel human diagnostic protein #7506.
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23-AUG-2000; 2000US-00649167.
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Best Local Similarity 97.5%;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed penes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II) is useful for generating antibodies against it, detecting or quantitating a
of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent din not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                   1969 AACACATAAAAAAGAGAGAAGAATCAAATAGACACAATAAAAAATGATAAAGGGGATAT
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                                                                                                                                                                                                                                                                                     5.5%; Score 115.2; DB 5; Length 1167; 97.5%; Pred. No. 3.7e-16;
                                                                                                                                                                                                                                                 Sequence 1167 BP; 492 A; 264 C; 202 G; 209 T; 0 U; 0 Other;
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polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
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Human, chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss DNA encoding novel human diagnostic protein #11170. AAS75366 standard; cDNA; 1167 BP (first entry) 13-FEB-2002 AAS75366; AAS75366/

Search completed: September 8, 2005, 23:49:42 Job time: 743.572 secs

10-MAR-2001, 2001WO-US008631 31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167 WO200175067-A2 11-OCT-2001

Homo sapiens

(HYSE-) HYSEQ INC.

WPI; 2001-639362/73. Drmanac RT, Liu C, P-PSDB; ABG11179

Tang YT

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 1; SEQ ID NO 11170; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal

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activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent directly from NIPO at
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Novel RNA biomarkers for diagnosis, prognosis and management of prostate, breast and bladder cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UROC-) UROCOR INC
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-MODEL=frame+ n2p.model -DEV=x1h
-MODEL=frame+ n2p.model -DEV=x1h
-G-CgnZ_1/USF7C_spool/USG9974546/runat_07092005_174357_19482/app_query.fasta_1.4942
-G-CgnZ_1/USF7C_spool/USG9974546/runat_07092005_174357_19482/app_query.fasta_1.4942
-DEA_Geneseq_16Dec04 -QFMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0
-LOST=45 -DOCALIGN=200 -THR_SCORE=pert -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL_-OUTFNT=pto -NORM*ext_-HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09974546_@CGN_1 1_232_@runat_07092005_174357_19482 -NCPU=6 -ICPU=3
-NO_MARP -LARGEQUERY -NEG_SCORE=0 -WAIT -DSPBELOK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREAPSIZE -SCORE=0 -LOURD=0 -LONGLOG
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOPE -DELEXT=7
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Abg17531 Abg17531 Abg17531
                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                 protein search, using frame_plus_n2p model
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                                                                                                                                                                                                                                                                                                                                                            2105692 seqs, 386760381 residues
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The invention provides nucleic acid markers of prostate, breast and bladder cancer. The markers are indicators of malignant transformation of prostate, breast and bladder tissues and are diagnostic of the potential for metastatic spread of malignant prostate tumours. The nucleic acid can also be used as targets for therapeutic intervention in prostate cancer. The cancer prostatic hyperplasia (BPH), bladder cancer or breast cancer. The markers may be used to design specific probes and primers, for the rapid analysis of prostate, bladder or breast biopsy samples. The probes and cerection and diagnosis. They may also be used to identify and isolate thill length gene sequences form various DNA libraries. Antibodies against the polypeptide products of the markers can be used to treat prostate cancer. Diadder cancer or breast cancer. The encoded proteins may be used to detect antibodies. The proteins and antibodies cancer in the proteins and matibodies may also be used for immunodetection methods for detecting or quantifying the cancers, and for clinical diagnosis of these cancers. The encoded proteins
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99WO-US013151 98US-00097199

WO9964631-A1 16-DEC-1999 (UROC-) UROCOR INC

12-JUN-1998; 11-JUN-1999;

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Nucleic acid marker; biomarker; tumour; prostate cancer; bladder cancer; benign prostatic hyperplasia; BPH; breast cancer; human; immunodetection

Homo sapiens

Prostate disease marker UC Band #28 amino acid sequence

(first entry)

19-APR-2000

AAY59295;

AAY59295 standard; peptide; 135 AA

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The invention provides nucleic acid markers of prostate, breast and bladder cancer. The markers are indicators of malignant transformation of prostate, breast and bladder tissues and are diagnostic of the potential for metastatic spread of malignant prostate tumours. The nucleic acid can also be used as targets for therapeutic intervention in prostate cancer. Denign prostatic hyperplasia (BPH), bladder cancer or breast cancer. The markers may be used to design specific probes and primers, for the rapid analysis of prostate, bladder or breast biopsy samples. The probes and primers may also be used for in situ hybridization or in situ PCR cancer, bladder or breast biopsy samples. The probes and cancer and diagnosis. They may also be used to identify and isolate full length gene sequences form various DNA libraries. Antibodies against the polypeptide products of the markers can be used to treat prostate cancer, bladder cancer or breast cancer. The encoded proteins may be used to detection methods for detecting or quantifying the cancers, and for clinical diagnosis of these cancers. The antibodies may also be used for radioimaging to quantify and localize the encoded proteins
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                                                                                                                                                                                                                                                             Novel RNA biomarkers for diagnosis, prognosis and management of prostate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 Gln11eArgLysLeuArgHisArgLeuSerAsnPheProArgLeuProGJy11eLeuAla
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                                                                                                                                                                             O'hara SM,
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-MODEL=frame+ n2p.model -DEV=xlh
-Q=/Cqn2 1/USPFO spool/18039974546 frunat 07092005 174359 19522/app_query.fasta_1.4942
-Q=/Cqn2 1/USPFO spool/18039974546 frunat 07092005 174359 19522/app_query.fasta_1.4942
-DB=ISBUGA_PATENTG AA -QFWT=fastan -SUFFIX=n2p.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=Dits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODEL-LOCAL -OUTFWT=pto -NORM=ext - THR_APPIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=USO9974546 @CGN 1 1 42 @runat -07092005 174359 19522 -MCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 86, Appl
Sequence 7461, Ap
Sequence 56, Appl
Sequence 6, Appli
Sequence 135, Ap
Sequence 12, Appli
Sequence 12, Appli
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                              - protein search, using frame_plus_n2p model
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US-09-097-199-86
US-09-513-9990-7461
US-09-097-199-56
US-08-477-451-6
US-09-134-0011-4352
US-08-477-451-18
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US-09-309-572-7
US-09-718-096-7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Patent No. 6218529
GENERAL IPPRMATT: An. Gang
APPLICANT: Al., Gang
APPLICANT: Ralph, David
APPLICANT: Ralph, David
APPLICANT: Veltri, Robert
TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
TITLE OF INVENTION: PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CARRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
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PROCR APPLICATION DATA:
APPLICATION NUMBER: 08/692,787
FILING DATE: 31-UL-1996
ATTORNEY/AGENT INFORMATION:
NAME: NAKENDAMEN: P-42,023
REFERENCE/DOCKET NUMBER: URC:018
TELECOMULNICATION INFORMATION:
TELEPHONE: (512) 414-300
TELEPAX: (512) 474-757
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
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Sequence 86, Application US/09097199
GENERAL INFORMATION:
APPLICANT: An, Gang
APPLICANT: O'Hara, S. Mark
APPLICANT: Veltri, Robert
TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
TITLE OF INVENTION: PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,199
                                                                                                                   Conservative:
Mismatches:
                                                                                                                                                                                                                US-09-974-546C-83 (1-2088) x US-09-097-199-84 (1-135)
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                                                                                 Length:
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CITY: Houston STATE: Texas
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,787
FILING DATE: 31-JUL-1996
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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; MOLECULE TYPE: protein US-09-097-199-84
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Best Local Similarity:
Query Match:
DB:
                                                        Alignment Scores:
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Sequence 84, Application US/09974546
Publication No. US20030050470A1
GENERAL INFORMATION:
APPLICANT: An, Gang
O'Hara, S. Mark
Ralph, David
Veltri, Robert
TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
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US-09-974-546-86

US-10-002-2546-86

US-10-002-828-15-189

US-11-057-807-257

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US-11-057-807-257

US-10-085-189

US-10-114-270-30

US-10-114-270-30

US-10-114-270-30

US-10-114-270-30

US-10-085-198-156

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US-10-189-437-494
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CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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COUNTRY: USA
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Match 1
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-MODEL=frame+ n2p.model - DEV=xlh
-Q=/Cgn2 1/USPTO spool/US09974546/runat_07092005_174400_19612/app_query.fasta_1.4942
-Q=/Cgn2 1/USPTO spool/US09974546/runat_07092005_174400_19612/app_query.fasta_1.4942
-D=Published Applications AA -QFWT=fastan -SUFFIX=n2p.rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pto -NORM=ext -HEARSTZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09974546 @CGN 1 1 229 @runat_07092005_174400_19612
-NCPUS = ICPU=3 -NO MMAP -LARGEQUERY -NEG GCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMBOUT=120 -WARN TIMBOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                 8; Search time 117.944 Seconds (without alignments) 13965.459 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/Per_NEW PUB.pep:*
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Compugen Ltd
                                                                                                                              protein search, using frame_plus_n2p model
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GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0
Fgapop 6.0
Delop 6.0
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Database :

86, Appl 33, Appl 150, Appl 150, App 115, App 115, App 115, App 115, App 64, Appl 226, Appl 235, App 326, Appl 335, Appl 335, Appl 326, Appl 327, Appl 326, Appl 327, Appl 326, Appl 327, Appl 327, Appl 326, Appl 327, Appl 326, Appl 327, Appl 326, Appl 326, Appl 327, Appl 326, Appl 326,

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Scoring table:

153, App 189, App 257, App 257, App 3, Appli 34, Appli

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Description

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56, Appl 15035, A

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20398, A

Sequence Sequence Sequence Sequence

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US-09-974-546C-83 (1-2088) x US-09-974-546-86 (1-135)
                                                                     NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (512) 474-7577
                                                                                                                   STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 86:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             694.00
100.00%
100.00%
                                                                                                                                CITY: Houston
                                                                                                                                                             COUNTRY: USA
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Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGATCAGAAAATTGAGGCACAGATTAAGTAACTTCCCAAGGCTACCAGGCATTCTAGCT
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: R09/974,546
FILING DATE: 10-Oct-2001
CLASSIFICATION: UNKnown
PRIOR APPLICATION: UNKnown
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATE: 1999
FILING DATE: 1998-06-12
ATTORNEY/AGRIT INFORMATION:
NAME: NAME: 1998-06-12
ATTORNEY/AGRIT INFORMATION:
REGISTRATION NUMBER: P-42,023
REFERENCE/DOCKET NUMBER: UROC:018
TELEPHONE; (512) 414-3500
TELEPAX: (512) 414-7577

INPORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGHIL: 335 amino acids
LENGHI: 135 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CysCysLeuLeuTyrLeuSerLysThrIleHisProGlnIleIle 135
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Matches:
Conservative:
Mismatches:
Indels:
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SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 86, Application US/09974546
Publication No. US20030050470A1
GENERAL INFORMATION:
APPLICANT: An, Gang
O'Hara, S. Mark
Ralph, David
                                                                                                                                                                                                                                                                                                                                                                                                                                     7.85e-71
694.00
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Best Local Similarity:
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Pred. No.:
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US-09-974-546-86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       279 AGAAGTCAAAAGGCAACAGAGTTCATTGATTATTCCATAGAACAGTCACCATGCAATT
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Veltri, Robert
TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 ATGAGGGCCTTCTTAAGGAACCAGAATATGAGGATATGCACAATATTATTCACAT
                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDTUM TYPE: FLOPPY disk

MEDTUM TYPE: FLOPPY disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/974,546

FILING DATE: 10-Oct-2001

CLASSIFICATION: UNKnown

PRIOR APPLICATION UNKnown

PRIOR APPLICATION NUMBER: 09/097,199

TILING DATE: 1998-066-12

ATORNEY/AGENT INFORMATION:

NAME: NAKASHIMA, RICHARG A.

RECISTRATION NUMBER: P-42,023

REFERENCE/DOCKET WUMBER: UROC:018

TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
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5.1.6
Compugen Ltd.
 GenCore version
Copyright (c) 1993 - 2005
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- protein search, using frame_plus_n2p model OM nucleic

9, 2005, 09:43:33 September Run on:

3; Search time 25.2251 Seconds (without alignments) 15928.642 Million cell updates/sec

US-09-974-546C-83 3589

1 gaccttaaatatatcgaggt......... Perfect score: Sequence:

BLOSUM62 Scoring table:

0.5 7.0 7.0 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

283416 seqs, 96216763 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2: model -DEV=xlh
-MODEL=frame+ n2: model -DEV=xlh
-MODEL=frame+ n2: model -DEV=xlh
-Cap.Z 1/USFTO_spool/US09974546/runat_07092005_174358_19508/app_query.fasta_1.4942_-D=CGDZ_1/USFTO_spool/US09974546/runat_07045-0.1 -LOOPCL=0 -LOOPCXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-UOCALIGN=200 -THR_SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-UOTRWT=pto -NORN=ext -HEAPSTZE=56 -MINELEN=0 -MAXLEN=200000000
-USER=US09974546 @CGN 1 1.79 @runat_07092005_174358_19508 -NCPU=6 -ICPU=3
-NO_MARP -LARREQUERY -NEG_SCORES=0 -WAIT -DSSPBLOK=100 -LONGIOG
-DEV IIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

Database :

PIR_79:* 1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

hypothetical prote probable hexosyltr hypothetical prote retrovirus-related retrovirus-related hypothetical prote lamin-like protein retrovirus-related retrovirus-related probable reverse t line-1 protein ORF reverse transcript reverse transcript probable RNA-direc Description SUMMARIES B34087 I59767 A26718 B28096 I38588 S65824 GNHUL1 B25556 GNMSLL GNLRL1 316783 B 8 1275 1275 1275 1280 138 335 1260 190 Length Query 197 197 197 195 187 171.5 156 Result No.

antigen 7H8/7 - ma	hypothetical prote	probable vacuolar	tumor necrosis fac				hypothetical prote	genome polyprotein	two-component sens	23S rRNA intron 2	conserved hypothet	protein g377 - mal	hypothetical prote	hypothetical prote	hypothetical prote	general sporulatio	hypothetical prote			hypothetical prote	reverse transcript	hypothetical prote	DNA-directed RNA p	probable ubiquitin	ORF MSV224 probabl	hypothetical prote	hypothetical prote	two-component sens	guanine nucleotide	hypothetical prote
D60396	A82069	T37840	GORTT1	T40355	D86322	T25821	C75006	RRXPLC	D70045	206607	D64555	T18414	H90124	B71619	F86174	S52674	T21204	B90095	AH2184	G90115	T14855	A99106	RNLVC2	B84611	T28385	T25819	AG2349	AD1263	H90093	D90124
82 2	263 2	536 2	461 1	1136 2	399 2	367 2	379 2	2210 1	451 2	459 2	523 2	3119 2	753 2	2539 2	645 2	698 2	367 2	472 2	599 2	196 2	1258 2	731 2	1386 1	365 2	833 2	380 2	434 2	479 2	680 2	706 2
5.6	5.6	2.6	2.5	2.5	2.5	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.2	•	2.5	2.5	2.5
94	92.5	92	91.5	90	89.5	87.5	87	87	86.5	86.5	85.5	85.5	82	85	84.5	83	82.5	82.5	82.5	82	82	81.5	81.5	81	81	80.5	80.5	80.5	80.5	80.5
15	16	17	18	c 19	20	c 21	22	23	24	25	56	27	c 58	29	30	31	c 32	33	34	c 35	36	37	38	39	40	c 41	42	43	C 44	45

ALIGNMENTS

Cispecies: Homo sapiens (man)
Cibate: 03-Nov-1988 #text_change 09-Jul-2004
Cibate: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 09-Jul-2004
Cibate: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 09-Jul-2004
Riskowronski, J.; Fanning, T.G.; Singer, M.F.
Mol. Cell. Biol. 8, 1385-1397, 1988
A;Title: Unit-length line-1 transcripts in human teratocarcinoma cells.
A;Reference number: A28096; MulD:88246405; PMID:2454389
A;Reference number: A28096; MulD:88246405; PMID:2454389
A;Reference number: Daso96
A;Reference repeal manay; not compared with conceptual translation
A;Rolecule type: mRNA
A;Residues: 1-1775 cSNO>
A;Cross-reference: UNIPROT:015604; UNIPROT:09UN80; UNIPROT:012881; UNIPROT:000363; UNIPROT:000375
C;Superfamily: pol polyprotein line-1 protein ORF2 - human

1275 37 0 0 0 0 Matches: Conservative: Mismatches: Length: Indels: 197.00 100.00% 100.00% 5.49% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match: DB: Score:

US-09-974-546C-83 (1-2088) x B28096 (1-1275)

1976 AAAAAAAGAGAGAAGAATCAAATAGACACAATAAAAAATGATAAAGGGGGATATCACCACC 2035 ò 셤

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CyAccession: A2513
RyHattori, M.; Kuhara, S.; Takenaka, O.; Sakaki, Y.
Nature 321, 625-628, 1986
A;Title: Li family of repetitive DNA sequences in primates may be derived from a sequence A;Title: Li family of repetitive DNA sequences in primates may be derived from a sequence A;Tatle: Li family of repetitive DNA sequences in primates may be derived from a sequence A;Status: conceptual translation of pseudogene
A;Status: conceptual translation of pseudogene
A;Status: conceptual translation of pseudogene
A;Nolecule type: DNA
A;Residues: 1-1259 cHMT>
A;Cross-references: UNIPROT: P08547
A;Cross-references: UNIPROT: P08547
A;Note: this sequence was constructed from an alignment of published and unpublished sequence cykeywords: reverse transcriptase; pseudogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1663 CAAACTIGITRGAICAACCICCAACAAGACAACAITCAGGAGITAAATATITITCAICAA 1722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1723 ACATTGGATTTTTCCTTAACGCTAGAGATTGCTACAAATCTTCTGAAGGGTCTCAATGGC 1782
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B34087
hypothetical protein (L1H 3' region) - human
hypothetical protein (man)
C;Species: Homo sapiens (man)
C;Species: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 09-Jul-2004
  C;Date: 31-Mar-1988 #sequence_revision 04-Jan-1996 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             279 LysAspThrThrTyrGlnAsnLeuTrpAsp-----ThrAlaLysAlaValCysArgGly
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315 ThrLeu---IleSerGlnLeuLysGluLeuGluLysGlnGluGlnThrAsn-SerLysAl
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Conservative:
Mismatches:
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                                          C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: 138588
R;Holmes, S.E.; Dombroski, B.A.; Krebs, C.M.; Boehm, C.D.; Kazazian, H.H.
Nature Genet. 7, 143-148, 1994.
A;Title: A new retrotransposable human L1 element from the LRE2 locus on chromosome 1q p
A;Reference number: 138588
A;Residues: 1.1275 cRES
A;Residues: 1.1275 cRES
A;Cross_references: UNIRROT:Q12881; EMBL:U09116; NID:g483914; PIDN:AAB60345.1; PID:g4839C;Superfamily: pol polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule_type: DNA_
*Residues: 1-1275 <DOM>
A;Cross-references: UNIPROT:Q15604; EMBL:M80340; NID:g339767; PIDN:AAA51622.1; PID:g3397
C;Superfamily: pol polyprotein
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C;Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S65824
R;Dombroski, B.A.
R;Dombroski, B.A.
Submitted to the EMBL Data Library, January 1992
A;Description: Isolation of an active human transposable element.
A;Reference number: S65823
reverse transcriptase homolog - human retrotransposon L1
NyAlternate names: ORP2 protein
C:Species: Homo sapiens (man)
C:Species: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
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retrovirus-related reverse transcriptase pseudogene - human
C;Species: Homo sapiens (man)
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A; Status: preliminary
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Q6qi76 P08548 Q63501

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O9qui2 O9qwy0 P11369 O08906

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099wy3 06txj1 062658 091z89 07r7b9 06qi35

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Q6q158

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Q6txe2 Q63288 Q6tuf6 Q9qym3

musculu

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SEQUENCE FROM N.A.

TISSUB=Prostate cancer;

MEDLINE=21028101; PubMed=11156405;

MEDLINE=21028101; PubMed=11156405;

MIG., Ng. A.Y., Meka C.S.R., Luo G., Bright S.P., Cazares L.,

Wright G.L. Jr., Veltri R.W.;

"Cloning and characterization of UROC28, a novel gene overexpressed in prostate, breast, and bladder cancers.";

PROSTATE TO 7014-7020(2000).

EMBL; AF1892209; AAG17118.1; -.
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Catarrhini, Hominidae, Homo.
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Matches:
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SEQUENCE 135 AA; 15722 MW;
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Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
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01-MAR-2001 (TrEMBLrel. 16,
05-UUL-2004 (TrEMBLrel. 27,
UC28 protein.
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Copyright (c) 1993 - 2005 Compugen Ltd.
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372 LysileAspArgProLeuAlaArgLeuIleLysLysLysArgGluLysAsnGlnIleAsp 391
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MEDLINE=97285120; PubMed=9140393;
Sassaman D.M., Dombroski B.A., Moran J.V., Kimberland M.L., Naas T.P.,
Sassaman D.M., Dombroski B.A., Swergold G.D., Kazazian H.H. Jr.;
DeBerardinis R.J., Gabriel A., Swergold G.D., Kazazian H.H. Jr.;
"Many human L1 elements are capable of retrotransposition.";
Nat. Genet. 16:37-43(1997).
BMBL, 109372; AAC51276.1;
PIR; B28096; B28096.
PIR; S23650; S23650.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
GO; GO:00015740; F:RNA-directed DNA polymerase activity; IEA.
GO; GO:0016278; P:RNA-dependent DNA replication; IEA.
InterPro; IPR005135; Exo_endo_phos.
InterPro; IPR000477; RVTse.
Pfam; PF03772; Exo_endo_phos; 1.
Pfam; PF00078; RVT_1; 1.
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Homo sapiens (Human).
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N. Many human L.I. alementa are capable of retrotransposition."; PRIS, 182096; B28096.

N. MacSilland, U93570; AACSILRA: P. N. N. N. Alementa are capable of retrotransposition."; PRIS, 223650.

N. MacSilland, M
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pfam; PF03372; Exo_endo_phos; 1.
RNA-directed DNA polymerase; Transferase.
SEQUENCE 1275 AA; 149110 MW; 4711B3BC22F7674B CRC64;
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01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Query Match DB:

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000372

RESULT 2

us-09-974-546c-83.rge

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/codon_start=1
/product="UC28 protein"
/protein_id="AAG17118.1"
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/translation="WRAFLENQKYEDMHNIHILQIRKLRHRLSNFPRLPGILAPETV
LLPPCYKVFRKKEKVKRSQKATEFIDYSIEQSHHAILTPLQTHLTWKGSSMKCSSLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2103)
An,G., Ng,A.T., Meka,C.S., Luo,G., Bright,S.P., Cazares,L.,
Mright,G.L. Jr. and Veltri,R.W.
Cloning and characterization of UROC28, a novel gene overexpressed
in prostate, breast, and bladder cancers
Cancer Res. 60 (24), 7014-7020 (2000)
                                                                                                                                                                                                                                                                                                                                                              2103 bp mRNA linear
Homo sapiens UC28 protein (UC28) mRNA, complete cds.
AF189270
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1. .2103
1. .2103
/gene="UC28"
99. .506
/gene="UC28"
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Submitted (23-SEP-1999) UroSciences, U
Parkway, Oklahoma City, OK 73104, USA
Location/Qualifiers
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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="texan:9606"

/chromosome="6"

/map="6q23-q24"
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                                                    HSAC001642
                             AC125609
AC027715
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AC147280
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AC091928
AC004610
                                                                           AP000838
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                                                                                                                                  AL499602
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2 (bases 1 to 2103)
An,G. and Veltri,R.W.
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AR146835 Sequence
AR146836 Sequence
AR146836 Sequence
AL031433 Human DNA
AC036236 Homo sapi
BC065109 Homo sapi
AR146757 Sequence
AC131318 Mus muscu
AC026382 Mus muscu
AC026382 Mus muscu
AC053487 Homo sapi
AC17430 Homo sapi
AC17431 Homo sapi
AC06826 Homo sapi
                                                                         9; Search time 6016.29 Seconds (without alignments)
16916.746 Million cell updates/sec
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         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                 4708233 seqs, 24227607955 residues
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Maximum Match 100%
Listing first 45 summaries
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AF189269
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BC069109
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AC131318
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PRI 22-MAR-2001

UroCor, Inc., 840 Research

Homo sapien 118 Homo sapi 99 Homo sapi 196 Homo sapi 180 Pan trogl 138 Homo sapi 10 Homo sapi 10 Homo sapi 66 Human DNA

AC147280 E AC025538 F AC091928 F AC004610 F

AL450466 F AL357556 F AL596214 F AC145092 E

AC100799 PAC078936

Homo sapi Homo sapi Homo sapi Homo sapi Homo sapi Homo sapi

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2087; Conservative 0; Mismatches
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            1961. .2103
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1981 AAGAGAAAGAATCAAATAGACACAATAAAAATGATAAAGGGGATATCACCACCGATCC 2040 2041 CACAGAAATACAAACTACCATCAGAGAATACTACAAACACCTCTACGC 2088 	AR146835 2087 bp DNA linear PAT 08-AUG-2001 Squence 83 from patent US 6218529. AR146835.1 GI:15110024 ÜKROWN.	Unclassified. 1 (bases 1 to 2087) An,G., O'Hara,S.Mark., Ralph,D. and Veltri,R. Biomarkers and targets for diagnosis, prognosis and management of prostate, breast and bladder cancer Patent: US 621829-A 317-APR-2001; Location/Qualifiers	12087 /organism="unknown" /mol_type="unassigned DNA"	Query Match 99.4%; Score 2076; DB 6; Length 2087; Best Local Similarity 100.0%; Pred. No. 0; Matches 2087; Conservative 0; Mismatches 0; Indels 1; Gaps 1.	1 GACCTIAAAIAITCGAGGGGGAATTGATGIAIAATAATTTACAAAAITATTCTTCTA 60 [61 TIGCTACAGACTACAATTTACAGTAGGCCACCATGAGGCCTTCTTAAGGAACC 120 121 AGAAATATGAGGATATGACATATTTACAGATTTTACAGATCGAGAAAATTGAGGCACA 180	181 GATTAAGTAACTTCCCAAGGCTACCAGGCATTCTAGGCAAACTGTGCAAACTGTGCAT 240 181 GATTAAGTAACTTCCCAAGGCTACCAGGCATTCTAGCTCCAGAAACTGTGCTCTTACCAT 240 181 GATTAAGTAACTTCCCAAGGCTACCAGGCATTCTAGCTCCAGAAACTGTGCTCTTAACAT 240	AGAGT AGAGT	301 TCATTGATTATTCCATAGAACAGTCACACCATGCAATTCTCACACCCTTGCAGACACACT 360 	361 IGACCATGAAAGGTTCCTCAATGAAATGTTCCTCATTATCTTCAGAAGCCATATTATTCA 420 	421 CATTGACTTTGCAGTTAACTCAGACCCTAGGTCTGGAATGCTGTCTTCTCTACTTATCCA 480	AACTATACATCCACAGATCATATAAACTCTCAGCCCTGCTGCAAAGCCTTTCCAGAAAAACTCTCAGCCCTGCAAAAGCCTTTCCAGAAAAAAAA	ATAAAAATGGTTGAAAAGGCAATTCTGCTACCAATGACTGTTTAAGCCCAGCCAAGTAAC	カイカインとは、1の方が大きなのである。1、1、1ので、1分でしたが、1のは、1、1が対してしてからして大きないができます。 げんしき かんかけいてん カイザリング カイザリング カイザリング カイザリング カイザリング カイザー・カイン カイブ カイブ カイブ カイザー・カイブ カイザー・カイザー・カイザー・カイザー・カイザー・カイザー・カイザー・カイザー・

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

E 1 (Sases I to 2512)

S An, G., Ng, A.Y., Meka, C.S., Luo, G., Bright, S.P., Cazares, L.,
Wright, G.L. Jr. and Veltri, R.W.

Cloning and characterization of UROC28, a novel gene overexpressed
in prostate, breast, and bladder cancers

E 2102B101

D 11156405

E 2 (Dases I to 2512)

S An, G. and Veltri, R.W.

Direct Submission

L Submitted (23-SEP-1999) UroSciences, UroCor, Inc., 840 Research
Parkway, Oklahoma City, OK 73104, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="0c28"
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                                                                                     1800 TTCTCCCTGTTATAAGCAGCAGAAGACAAATTAGCCATTTCACTCTCAAACTTCACTAATGA
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1 (bases 1 to 2505)
An,G., O'Hara,S.Mark., Ralph,D. and Veltri,R.
Biomarkers and targets for diagnosis, prognosis
prostate, breast and bladder cancer
Patent: US 62185.9-A 85 17-APR-2001;
Location/Qualifiers 10; 9: B Score 1950; D Pred. No. 0; 0; Mismatches DNA" 1. .2505 /organism="unknown" /mol_type="unassigned 93.4%; Query Match 93.4 Best Local Similarity 99.4 Matches 1967; Conservative 721 721 781 781 ò g ò g

08-AUG-2001

PAT

linear

DNA

2505 bp US 6218529.

AR146836 Sequence 85 from patent AR146836 AR146836.1 GI:15110025

LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT 4 AR146836

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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality; as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, BMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
                                                                                                                                      הסב/באת 12922 pp DNA linear PRI 04-MAR-2003
Human DNA sequence from clone RPI-171N11 on chromosome 6q23,
complete sequence.
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Further information can be found at http://www.sanger.ac.uk/HgP/Chr6

RPI-171N11 is from the library RPCI-1 constructed by the group of Pieter de Jong. Por further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 129227)
1920 CTAACCATCTGAAGAAACTTCCCAAGTGTAAGACTTCTGCCATTAAAACATTACCGAGA 1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (04-MAR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBIO 18A, UK. E-mail enquirises the humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On May 13, 1999 this sequence version replaced gi:4582115.
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Web site: http://www.sanger.ac.uk
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/db_xref="taxon:9606"
/chromosome="6"
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/clone="RP1-171N11"
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                                  841 GCTCCGCTAGGCACCAGGGGATAAAAACAATACTTATAGTATACCACTAATTTCGCTT
                                                                                                                                            901 AGTAACTAGTGAAATGTTCAAGTCATGCCTGAGTCAAGAGTTGAGGAGACATTACAATGT
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29796 GACCTTAAATATCGAGGTGGCTAATTGATGTATAATAATTTACAAAATTATTCTT 29855 61 TTGCTACAGAGCTACAATTTACAGTAGGCCACCATGAGGGCCTTCTTAAGGAACC 120 61 TTGCTACAGAGCTACAATTTACAGTA-GTAAAGGAGCCACCATGTAAAGGAACC 120 62 9856 - TGCTACAGAGGTACAATTACAATTA-GTAAAATAAAGGAGCCCTTCTTAAAAGGAACC 120	AGAAATAGGGGATATGCACAATATTATCACATTTTACAGATCAGAAATTGAGGCACA	GATTAAGTAACTTCCCAAGGCTACCAGGCATTCTAGCTCCAGAACTGTGCTCTTACCAT GATTAAGTAACTTCCCAAGGCTACCAGGCATTCTAGCTCCAGAAACTGTGCTCTTACCAT	241 TCTGCTACAAGGTATTTCGAAAAAAGAAAAAGGTAAAAAGAAGGTCAAAAGGCAACAGGT 300 	301 TCATTGATTATTCCATAGAACAGTCACATGCAATTCTCACACCCTTGCAGACACACT 360	361 TGACCATGAAAGGTTCCTCAATGAAATGTTCCTCATTATCTTCAGAAGCCATATTATTCA 420	421 CATTGACTTTGCAGTTAACTCAGACCCTAGGTCTGGAATGCTGTCTTCTCTACTTATCCA 480	481 AAACTATACATCCACAGATCATAAACTCTCAGCCCTGCAGAAAGCCTTTCCAGAAAA 540 	541 ATAAAAATGGTTGAAAAGGCAATTCTGCTACCAATGACTGTTTAAGCCCAGCCAG	601 TGAACCATTCCAACTTCAATTTACTTATGAAAAGAATTTGATGATGTAGGGGGTTATTTC 660 	661 AATTCTAAAATACAAACCCATGTTGATCTTTCTCAATCTTGAACTCATAGATTATTATCT 720 	721 ATTATCTCAATTTAGTTTGTTATCCTAGTGGGCCATTAAAAACTACCACATGTGTT 780 	781 TCTGTCTCTCCATTAGTCAATAACTAAAGGAGCAATTAGTAAGCCATGTGCCAGAT 840 	841 GCTCCGCTAGGCACCAGAGGATAAAAACAATACTTATAGTATACCACTAATTTTCGCTT 900 	901 AGTAACTAGTGAAATGTTCAAGTCATGCCTGAGTCAAGAGTTGAGGACATTACAATGT 960 	961 GTAATGGAAACCAAGGAAAGTGAAACTTTGGATAAGTGGGGGACTAGTGTATTTATATATT 1020 	1021 TAATTGATTTCTGACTCTATCGCCTCCAAACACAGATTGTGTTTTTCTTTGGTTT 1080 	1081 GTTTCTTCACTATGGGATCTTCTGTGCCCAGCACAGTGCCTGACACATAGAAACAATC 1140

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                                                                                                            St. Louis,
                   2 (bases 1 to 186698)
Waterston, R.H.
Direct Submission
Submitted (07-APR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Sep 1, 2000 this sequence version replaced gi:7523932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence. It currently consists of 7 conigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                         Center project name: H_MH013015

Center project name: H_MH013015

Center project name: H_MH013015

Sequencing vector: plasmid; 0¢
Chemistry: Dye-primer ET; 100¢ of reads
Chemistry: Dye-primer ET; 100¢ of reads
Chemistry: Dye-terminator Big Dye; 0¢ of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 18432 bases at least Q40
Consensus quality: 185064 bases at least Q20
Insert size: 177000; agarose-fp
Insert size: 177000; agarose-fp
Quality coverage: 5.57 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                           Center: Washington University Genome Sequencing Center Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
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4869: gap of unknown length
4869: gap of unknown length
4870 11657: contig of 6788 bp in length
11757: gap of unknown length
11758 28189: contig of 16432 bp in length
11890 28289: gap of unknown length
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11891 contig of 25052 bp in length
1181 contig of 48886 bp in length
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118281: gap of unknown length
118281: gap of unknown length
118281: gap of unknown length
118688: contig of 80354 bp in length
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/noce="assembly_name:Contig13"
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102428. .182781
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/note="assembly_name:Contig12"
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                                                                                                                                                                                                                61 TTGCTACAGAGCTACAATTCAATTTACAGTAGGCCACCATGAGGGCCTTCTTAAGGAACC
                                                                                                                                                                                                                                                                                                                     121 AGAAATATGAGGATATGCACAATATTATTCACATTTTACAGATCAGAAAATTGAGGCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159394 TCTGCTACAAGGTATTTCGAAAAAAGAAAAAGTAAAAAGAAAAGGAAGCAACAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159454 TCATTGATTATTCCATAGAACAGTCACACCATGCAATTCTCACACCCTTGCAGACACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 TGACCATGAAAGGTICCTCAATGAAATGTICCTCATTAICTTCAGAAGCCATATTAITCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159514 TGACCATGAAAGGTTCCTCAATGAAATGTTCCTCATTATCTTCAGAAGCCATATTATTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159874 ATTATCTCAATTTAGTTTGTTATTTATCCTAGTGGGCCATTAAAAACTACCACATGTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159934 TCTGTCTCTCCATTAGTCAATAACTAAACTAACGAGCAATTAGTAAGCCATGTGCCCAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCATTGATTATTCCATAGAACAGTCACACCATGCAATTCTCACACACCTTGCAGACACACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               721 ATTATCTCAATTTAGTTTGTTATTTATCCTAGGGCCATTAAAAACTACCACATGTGTT
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                                                                                                          1 GACCTTAAATATATCGAGGTGGCTAATTGATGATAATAATTTACAAAATTTATTCTTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                GATTAAGTAACTTCCCAAGGCTACCAGGCATTCTAGCTCCAGAAACTGTGCTCTTACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 TCTGCTACAAGGTATTTCGAAAAAAAGAAAAGTAAAAGAAGAAGTAAAAGGCAACAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATAAAAATGGTTGAAAAGGCAATTCTGCTACCAATGACTGTTTAAGCCCAGCCAAGTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGAACCATTCCAACTTCAATTTACTTATGAAAAGAATTTGATGTGTAGGAGGTTATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            661 AATTCTAAAATACAAACCCATGTTGATCTTTCTCAATCTTGAACTCATAGATTATTATCT
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                                                         Gaps
     DB 2; Length 186698;
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                                                      14;
  Score 1920.2;
Pred. No. 0;
1; Mismatches
92.0%;
ilarity 99.1%;
Conservative
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12477932
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AUTHORS
TITLE
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           1021 TAATTGATTTCTGACTCTATCATTGGCCTCCAAACACAGATTGTGTTTTTCTTTGGTTTT 1080
160174 TAATTGATTTCTGACTCTATCACTTGGCCTCCAAACACAGATTGTGTTTTTCTTTGGTTTT 160233
                                                                                                  160654 AAAACTCAGTAAGAATTATATTAGTCTGTTTGCAAAGTAGAAAAAGATTCTCATCACTCA 160713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160774 TTTTAGACACTTCCCTGCATTAACTGCACAAACAATATGTTTGCAAACTTGTTAGATCAA 160833
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                                                                                                                                                                                                                                            160354 TAGAACATCCAGAGTAAGTGATGAGGGCCTCTGCATTTATATGCGCTTAAATTAAGATTA 160413
                                                                                                                                                                                                                                                                                                           160414 TGTGAGAAAAGTTTAAAGACACTTAGTAGAGTGATTTTTGAAATATAGAACACTTGGAA 160473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160894 AACGCTAGAGATTGCTACAAATCTTCTGAAGGTCTCAATGGCTTCAGGCTAAGAAGAGA 160953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161014 ATCACATTCTTTCCAAAAGGAACTCTAGAAGACCAAATGCCCCGAGTTAAGAACATCAAA 161073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens prostate and breast cancer overexpressed 1, mRNA (cDNA clone IMAGE:7216926).

BC069109
BC069109.1 GI:46575743
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                                                                            1081 GITITCTTCACTATGGGATCTTCTGTGCCCAGCACAGTGCCTGACACATAGAAAACAATC 1140
                                                                                                                                             1141 -AATATTTGCTGAATAAATGATTAAAAATCAGAGAACTTTCCCATTCTGTTTGGATCTA 1199
                                                                                                                                                                                                             TAGAACATCCAGAGTAAGTGATGAGGGCCTCTGCATTTATATGCGCTTAAATTAAGATTA 1259
                                                                                                                                                                                                                                                                            1260 TGTGAGAAAAGTTTAAAAGACACTTAGTAGAGTGATTTTGAAATATAGAAAACACTTGGAA 1319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCATATATTTTTACCATCTGCTGAAGGCAGTCATATCAAAGGGTAAAGAAGATGGGAGG 1499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1560 ACCTTATGAGCAGGAAGAGGCAGGATGTTTGAGAACCATTTACTTAGCAGAACCACATA 1619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1620 TTTTAGACACTTCCCTGCATTAACTGCACAAACAATATGTTTGCAAACTTGTTRGATCAA 1679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTCCAACAACGACACATTCAGGAGTTAAATATTTTTCATCAAACATTGGATTTTTCCTT 1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACGCTAGAGATTGCTACAAATCTTCTGAAGGGTCTCAATGGCTTCAGGGCTAAGAAGAGA 1799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1800 TITCICCCTGITATAAGCAGCAAGAAATAAGCCAITICACTCTCAAACTICACTAATG 1859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCACATTCTTTCCAAAAGGAACTCTAGAAGACCAAATGCCCCGAGTTAAGAACATCAAA 1919
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ACCESSION VERSION

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Mammalia; Eutheria; Craarrhin; Hominidae; Homo.

Is (bases 1 to 2456)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Rlausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopking, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Ugdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

N. Paror, Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: Plate: Row: Column: 0.
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                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (16-APR-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 IGCTACAGAGCTACAATTCAATTTACAGTAGGCCACCATGAGGGCCTTCTTAAGGAACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Anup Madan, University of Iowa
CDNA Library Preparation: Anup Madan, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
CDNA Sequencing by: Neurogenomics Research Lab,
anup-madan@ulowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ښ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Best Local Similarity 99.1%; Pred. No. 0;
Matches 1960; Conservative 1; Mismatches
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/organism="Homo sapiens"
/mol_type="mRNR"
/db xref="t=xon:9606"
/clone="IMAGE:7216926"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 2496)
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Homo sapiens
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126 GTGGGAAAGTTAAAGGCCTCTGGATTATATATATATATAT	∑ 0
122 GAMERITCH GRAFFING CONTINUED	TATTCTTCACTATGGGAAGTGAAAGTTGGGATAGTGGGACTAGTGTATTTTTTTT

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Lindblad-Toh,K., Liu,X., Lui,A., Mabbitt,R., MacLean,C.,
Macdonald,P., Major,J., Manning,J., Matchews,C., McCarthy,M.,
Macdonald,P., Meneus,L., Mihova,T., Mlanga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schubback,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiltev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Direct Submission
Submitted (20-FEB-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 20, 2004 this sequence version replaced gi:29150479.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
Http://ftp.genome.washington.edu/RM/RepeatMasker:html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125132 GAATTCTAGAACATTCACAGTAAATGCTGAG-----AGCTTACATCTGTGCTTAACTTC 125185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1194 GATCTATAGAACATCCAGAGTAAGTGATGAGGCCCTCTGCATTTATATGCGCTTAAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Pred. No. 2.8e-15;
1; Mismatches 244; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L26968
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of 24759 bp in length
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of 26234 bp in length
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of 14696 bp in length
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contig of 33844 bp in length
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/clone_lib="RPCI-23 Female Mouse BAC"
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/chromosome="10"
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196741: contig
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Best Local Similarity 59.3<sup>3</sup>
Matches 416; Conservative
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Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Cogulaviy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Cocum,B. DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafes,N., Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme, W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 230685)
                                                                                                                                                                                                                                                                                                                                                                                                                              181 TTCTTTCCAAAAGGAACTCTAGAAGACCAAATGCCCCGGGTTAAGAACATCAAAACTAAC
                                                                                                                                                                                                   1746 AGAGATTGCTACAAATCTTCTGAAGGGTCTCAATGGCTTCAGGCTAAGAAGAGATTCTC
                                                                                                                                                1 ACAACGACACTTCAGGAGTTAAATATTTATCATCAAACATTGGATTTTTCCTTAACGCT
                                                           Gaps
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       Length 757;
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Mus musculus chromosome 10 clone RP23-367D2 map 10,
                                                                                                    1686 ACAACGACATTCAGGAGTTAAATATTTTTCATCAACATTGGATTTT
                                                      Indels
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HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN
Mus musculus (house mouse)
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     Query Match 13.2%; Score 275.4; DB 6; Best Local Similarity 96.2%; Pred. No. 3e-42; Matches. 282; Conservative 0; Mismatches 11;
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
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AC131318
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41; Gaps

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Sequencing vector: M13; L08821
Sequencing vector: M13; L08821
Chemistry: Dye-terminator Big Dye: 4% of reads
Chemistry: Dye-terminator Big Dye: 4% of reads
Chemistry: Dye-terminator Big Dye: 4% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: L59501 bases at least Q40
Consensus quality: L69264 bases at least Q20
Consensus quality: L69264 bases at least Q20
Estimated insert size: L6920; sum-of-contigs estimation
Quality coverage: 4.5x in Q20 bases; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is
Direct Submission
Submitted (22-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Oct 14, 2001 this sequence version replaced gi:11094624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Games of the control are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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unknown length
of 6770 bp in length
unknown length
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                                                                                                                                                            Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-hely@bcm.tmc.edu
Center: project Information
Center project name: MADA
Center clone name: RP23-246G10
                                                                                                                                           Center: Baylor College of Medicine
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Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1. (Dases 1 to 167998)

Metzker, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C.,

Dederich, D., Thomas, S., Okwnonu, G., Carlock, C., Garner, T.,

Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J.,

Buhay, C., Burac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z.,

Cox, C., Davis, C., Delgado, D., Porcum-Tansey, J., Gill, R.,

Gorrell, J.H., Quanatane, P., Haller, G., Hernandez, J., Megues, M.,

Houx, Y., Huber, J., Jackson, L., Jia, Y., Kelly, S.,

Kovar, C., Liu, J., Liu, M., Loulseged, H., Lozado, R.J., Martin, R.,

Massey, E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Martin, S.,

Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Oguh, M., Parish, B.,

Millamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, R.,

Worley, K., and Gibbs, R.,

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .25708 GCTTACGGTAAGAAGGCCTTGCTTTGCCCCTTGATATAAGGAGGTAAACAACTCAGTCAT 125767
                                                                                                                                 125305 ACAAAGAGIGAATAAACGAAAGAAAATTTACAGTTATGGACTTCTGCATGTTTGCTTC 125364
                                                                                                                                                                                                                                                                                                                                                                                                            125472 C-TCAGTCAACATTAGCAGCAGGAA---GGAAAGCTGCCTAAAAACAAATTACTTAGGAG 125527
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                                                                                                                                                                                                                               125365 TTCT-----TTATAATCATCTGCCTAAGGTAGTTATTTCAAAGGGTAAA-AGA 125411
                                                                                                                                                                                                                                                                                                                   125412 GAAAGAAGAAAAATATAATTAGTATTGTATAAATGTGTGTGCCAGGTAGAAAAATCTTAT 125471
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                                                                                                                                                                                                                                                                               1491 GATGGGAGGAAAACTCAGTAAGAATTATATTAGTCTGTTTGCAAAGTAGAAAAAGATTCT 1550
                                                                                                                                                                                                                                                                                                                                                                        CATCACTCAACCTTATGAGCAGGAAGAGGCTGTTTGAGAACCATTTACTTAGCAG 1610
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Mus musculus clone RP23-246G10, WORKING DRAFT SEQUENCE, 19
unoxidered pieces.
1311 CACTIGGAAATGGTGGTGCTTTAAAAAGATATTAATAGATAATATGAAAATCTCCATCTC 1370
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                                                                                           GCAAACTTGTTRGAT-CAACCTCCAACAACGACACATTCAGGAGTTAAATATTTTTCATC
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AC026382.8 GI:16118081
HTG; HTGS PHASE; HTGS DRAFT.
Mus musculus (house mouse)
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Worley, K.C.
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Van Brunt, A. and Kozlowicz, A.
The sequence of Homo sapiens BAC clone RP11-721G13
The sequence of Homo sapiens BAC clone RP11-721G13
Waterston, R.H.
Waterston, R.H.
Direct Submission
Submitted (10-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
Materston, R.H.
Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (21-OCT-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                           54002 CAAAATTGATAGACCGCTAGCAAGATGACAAAGAAAAAAAGGAGAAGAATCAAATAGAC
                                                                                                                                                                                        54062 ACAATAAAAATGATAAAGGGGATATCACCACCGATCCCACGGAAATACAAACTACCATC
                                                                                  1943 CAAGTGTAAGACTCTGCCTGCACGACAACACATAAAAAAAGAGAGAAGAATCAAATAGAC
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AC093897 AC067901
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Center code: WUGSC
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    Length 110000;
                                           Indels
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Contact: sapiens@watson.wustl.edu
------- Summary Statistics
Center project name: H_NH0721G13
Drafting Center: WIBR
Score 122; DB 2;
Pred. No. 8.1e-14;
0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 163271)
Sulston,J.B. and Waterston,R.
Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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5.8%;
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Waterston, R.
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                                                                                                                                                                                                                                                                                                                                   1254 AGATTATGTGAGAAAAGTTTAAAG---ACACTTAGTAGAGTGATTTTGAAATATAGTAAA 1310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1721 AAACATTGGATTTTTCCTTAACGCTAGAGATTGCTACAAATCTTCTGAAGGGTCTCAATG 1780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTTCAGGCTAAGAAGAGA ---TTTCTCCCTGTTATAAGCAGCAAGACAAATTAGCCAT 1836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1669 IGTTRG-----ATCAACCTCCAACAACGACATATTTAAATATTTTTCATC 1720
                                                                                                                                                                                                                                                                                          51613 GAATICTAGAACATICACAGTAAATGCTGAG-----AGCTTACATCTGTGCTTAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1431 ATTACTTTTTCATATATTTTTACCATCTGCTGAAGGCAGTCATATCAAAGGGTAAAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                   1311 CACTIGGAAATGGTGGTGCTTTAAAAAGATATTAATAGATAATATGAAAATCTCCATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                             51786 ACAAAGAGTGAATAAACGAAAGAAAATTTACAGTTATGGACTTCTGCATGTTTGCTTC
                                                                                                                                                                                                                                                  1194 GATCTATAGAACATCCAGAGTAAGTGATGAGGGCCTCTGCATTTATATGCGCTTAAATTA
                                                                                                                                                                                                                                                                                                                                                             51846 TTCT------TTATAATCATCTCCTAAGGTAGTTATTTCAAAGGTAAATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52190 GCTTACGGTAAGAAGGCCTTGCTTTGCCCCTTGATAAAGGAGGTAAACAACTCAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCATCACTCAACCTTATGAGCAGGAAGAGGGAAGGCTGTTTGAGAACCATTTACTTAGCA
                                                                                                                                                                                                              Gaps
                                                                                                                                                                       Length 167998;
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                                                                                                                                                                                                           Indels
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                                                                                                                                                                  Score 123.2; DB 2;
Pred. No. 4.3e-14;
1; Mismatches 249;
                   1. .167998
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-246G10"
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                                                                                                                                                                Query Match
Best Local Similarity 58.7%;
Matches 412; Conservative
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Fragment Name Be
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AC114782 1
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AC114782 3 3
AC114782 4 4 4
Continuation (2 of 5) of 1
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WPCOMMENT
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FEATURES
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repeat_region
                                                                                                                                                                 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The clone sequenced to the right is AC019264. Actual start of this clone is at base position 1 of RP11-721G13; actual end is at base position 163271 of RP11-721G13.
chemistry, or covered by high quality data (i.e., phred quality >= 0.0); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                            The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pleter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Data from AC019264 and AC093652 was used to finish this clone AC093897. Polymorphisms have been identified between AC093652 and AC093897. Single plasmid region exists between 149738 and 149749.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence of AC067901 has been incorporated into AC093897.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="MER1_type"
3733. .3757
/rpt_family="AT_rich"
4460. .4510
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5475_ .5496
/rpt_family="AT_rich"
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1822_ 1879
/rpt_family="(TA) n"
2408_ 2568
2793_ 2971
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1. .213
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/rpt_family="CR1"
5168. .522
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/rpt_family="MIR"
3003. .3177
/rpt_family="MIR"
3182. .3395
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6886. .7074
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7177. 7326
/rpt_family="MIR"
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1362_ .1502
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/rpt_family="MIR"
.069. .1278
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/map="4"
                                                                                                                                               MAPPING INFORMATION:
                                                                                                                                                                                                                                                                                          SOURCE INFORMATION:
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                                                                                                restriction digest
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2547. .12839
note="similar to EST AA677976 (NID:92658498) zi14c09.sl"
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/noce="similar to EST BE833497 (NID:g10265875)"
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2957. .12989
rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                    rpt_family="MER1_type" 3962. .13982
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4808. .15206
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6051. .16096
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6098. .16512
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9048. .9329
                                                                                                                                                      rpt family="AT_rich" 0470. 1040
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4495. .14643
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0471. .10748
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1356. .21578
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3471. .23600
                                 rpt_family="(CA)n"
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3269. .23418
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23432. .23455
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2547. .12839
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/rot_family="L1"
9473. .9747
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/rpt_family="L2"
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3732. .23864
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5230. .25252
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10230. 1075
                                                                                                                                                                                                    /rpt_family="L1"
11055. .11???
                                                                                                                                                                                                                                                                                                                                                                                                                     family="MaLR"
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3583. .23616
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          /rpt_family="Alu"
8792. .8824
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. .15969
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7129. .17628
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                                                                                                             /="L1"=
                                                                                         /rpt_family="1757"
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5729.
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SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
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Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence
                                                                                           Submitted (10-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 154941)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Peatures listing.
                                                                                                                                                                                                                                                                                        Submitted (29-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (30-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 154941)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (27-UTN-2002) Human Genome Sequencing Center, Department
Subjectular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .2000
/note="overlaps bases 113280. .115279 of clone AC112506"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Apr 30, 2002 this sequence version replaced gi:20279244. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu
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/db_xref="taxon:9606"
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Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 114941)

Manziatus, Manas, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alaboroks, S.L., Amaratunge, H.C., Arc, J.R., Ayele, M., Banks, T., Barbaria, J., Barton, P., Baryan, P., Barbaria, J., Barcoks, S.L., Barcon, E., Burcoh, D., Burch, P., Chon, G., Chen, G., Dath, H., Delaney, K.R., Delgar, D., Denther, S.R., Davis, C., Davis, C., Davis, C., Burch, D., Datherne, S.R., Davis, C., Davis, C., Coyle, M. D., Delaney, K.R., Delgar, D., Edward, G. Garza, M., Gall, K., J., Davis, C., Edgar, D., Flagg, N., Ford, J., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Escotto, M., Falls, T., Gaveral, J., Garcia, M., Ganzala, M., Hele, X., Harrandez, J., Hernandez, O., Hadgeon, A., Hogues, M., Holloway, C., Hollins, B., Homai, F., Howard, S., Huber, J., Holloway, C., Katyoro, J., Ja, Y., Johnson, R., Holloway, C., Lewis, L., Li, J., Li, J., Li, J., Li, Lozado, R., Ludier, P., Haves, A., Lucier, R., Luna, S., Houle, S., Man, S., Man, J., Man, B., Lewis, L., Li, J., Li, J., Li, J., Li, Lozado, R., Lucier, J., Hulle, J., Man, J., Man, 
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         Length 163271;
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      Score 122; DB 9;
Pred. No. 7.3e-14;
0; Mismatches 15;
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5.8%;
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      Query Match
Best Local Similarity 89.7°
Matches 131; Conservative
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Direct Submission
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27131. :2720n
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complement(30330. 30426)
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complement(14404..14713)
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complement(18970. .24273)
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complement (24298. .25342)
/rpt_family="LIPB1"
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complement(28751. .29047)
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15149. 15255
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complement(26363..26
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16099. .26100
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29505. .29812
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147088
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2 (Dases I to 155722)
Waterston,R.H.

Submitted (16-ARR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
Mn 63108, USA
On Sep 1, 2000 this sequence version replaced gi:9795672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 155722) Waterston, R.H.
                                                                                                                                             147087 AAGACTAATAAAGAAAAAAGAGAAGAATCAAATAGACACAATAAAAAATGATAAAGGG
                                                                                                                                                                                         147147 AATTAATGAATCCAGGAGCTAGTTTTTGAAAGGATCAACAAAATTGATAAACTGCTAGC
                                                                                                                                                                                                                                           1964 ACGACAACACATAAAAAAGAGAGAAGAATCAAATAGACACAATAAAAATGATAAAGGG
                                                                                                                                                                                                                                                                                                                                       2024 GATATCACCACCGATCCCACAGAAATACAAACTACCATCAGAGAATACTACAAACACCTC
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consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
                                                                                                ö
                                             5.8%; Score 121; DB 9; Length 154941; 78.4%; Pred. No. 1.1e-13; ative 0; Mismatches 40; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Washington University Genome Sequencing Center Code: WUGSC
Web site.http://genome.wustl.edu/gsc/index.shtml
Center project Information
Center project name: H NH0119D18
Sequencing vector: M13; 76%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage: 8.60 in Q20 bases; agarose-fp
Quality coverage: 7.32 in Q20 bases; sum-of-contigs
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Chemistry: Dye-primer ET; 74% of reads
Chemistry: Dye-terminator Big Dye; 26% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 154612 bases at least Q40
Consensus quality: 1549798 bases at least Q30
Insert size: 132000; agarose-fp
Insert size: 134934; sum-of-contigs
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
Homo sapiens
repeat_region 30572. .30742
                                                                 Best Local Similarity 78.4 Matches 145; Conservative
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/standard_name="Restriction Fragment Length Polymorphism"
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Location/Qualifiers
1. .180388
                        235 (4794), 1394-1399 (1987)
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1858. .1863
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866. .1872
bound_moiety="ATF"
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Nature 353 (6339), 83-86 (1991)
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bound_moiety="SP1"
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/number=1
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Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
Human retinoblastoma susceptibility gene: cloning, identification,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Deletions of a DNA sequence in retinoblastomas and mesenchymal tumors: organization of the sequence and its encoded protein Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)

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as soon as it is available and the accession number will be preserved.
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                                      1 154934: contig of 154934 bp in length 5 155722: contig of 688 bp in length. Location/Qualifiers
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78083. 78279,149998. 150116,153208. 153353,156693. 156838,
160730. 160834,161997. 162110,162204. 162367,
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LFSKLERTCELI YLTQPSSSI STEI NSALVLKVSWI TFLLAKGEVLQMEDDLVI SFQL
MLCVLDYFI KLSPPMLLKEPYKTAVI PI NGSPRTPRRGQNRSAR I AKQLENDTRI I EV
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LPCHDIKTLOTDSI DSFETQRTPRKSNLDEBVNYI PPHTPWRYTWNTI OLOLMMILLNSA
SOPOSBNIL ISYFNNYTVNPKES I LKRVKDI OYI PKEKFARA VGGGCVBI GSQRYKLGY
RLYYRVMESMLKSEERELSI ONFSKLIANDNI PHMSLLACALEVVMATYSRSTSQNIDS
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4 (gites)
McGee,T.L., Yandell,D.W. and Dryja,T.P.
Structure and partial genomic sequence of the human retinoblastoma
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Toguchida, J., McGee, T.L., Paterson, J.C., Eagle, J.R., Tucker, S., Yandell, D.W. and Dryja, T.P.
Complete genomic sequence of the human retinoblastoma susceptibility gene Genomics 17 (3), 535-543 (1993)
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product="retinoblastoma susceptibility protein"
protein_id="AAA53483.1"
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Sequence 85, Appl
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           GenCore version 5.1.6
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Sequence 83, Application US/09097199

Fatent No. 6218529

Patent No. 6218529

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Patent No. 6218529

Patent No. 6218529

APPLICANT: An, Gang

APPLICANT: An, Gang

APPLICANT: Ralph, David

TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,

TITLE OF INVENTION: PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE

NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
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Sequence 15532,
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC Compatible
OPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,199
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/692,787
FILING DATE: 31-JUL-1996
ATTONEY/AGENT INFORMATION:
NAME: NARESHERCE/DOCKET UNMBER: P-42,023
REGISTRATION NUMBER: P-42,0
US-09-949-016-13527
US-09-949-016-12417
US-09-949-016-12415
US-09-949-016-12415
US-09-949-016-12754
US-09-949-016-12754
US-09-949-016-116730
US-09-949-016-116730
US-09-949-016-11855
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	; Pred. No. 0; 0, Indels 1; Gaps	1 GACCTIAAATATATCGAGGTGGCTAATTGATGTTATAATAATTTACAAAATTATTCTTCTA 60	61 TTGCTACAGAGCTACAATTTACAGTAGGCCACCATGAGGCCTTCTTAAGGAACC 	121 AGAAATATGAGGATATGACAATATTATTCACATTTTACAGATCAGAAAATTGAGGCACA	181 GATTAAGTAACTTCCCAAGGCTACCAGGCATTCTAGCTCCAGAAACTGTGCTCTTACCAT 	241 TCTGCTACAAGGTATTTCGAAAAAAAAAAGGTAAAAAGAAGTCAAAAGGCAACAGGT 	301 TCATTGATTATTCCATAGAACAGTCACACCATGCAATTCTCACACCCTTGCAGACACTCTTTCACAGACAG	361 TGACCATGAAAGGTTCCTCAATGAAATGTTCCTCATTATCTTCAGAAGCCATATTATTCA	421 CATTGACTTTGCAGTTAACTCAGACCCTAGGTCTGGAATGCTGTCTTCTACTTATCCA	481 AAACTATACCACGATCATATAAACTCTCAGCCCTGCTGCAAAGCCTTTCCAGAAA 481 AAACTATACGACGAATCATATAAACTCTCAGCCTGCTGCAAAAGCCTTTCCAGAAA 481 AAACTATACATCGACAATCATATAATAACTCTCAGCCTGCAAAGCCTTTCCAGAAAA	541 ATAAAAATGGTTGAAAAGGCAATTCTGCTACCAATGACTGTTTAAGCCCAGCCAAGTAAC	601 TGAACCATTCCAACTTACTTATGAAAAGAATTTGATGATGATGAGGAGGTTATTTC 601 TGAACCATTCCAACTTACAATTACTTATGAAAAGAATTTGATGATGATGATGATGATGATGATG	661 AATTCTAAAATACAAACCCANGTTGATCTTTCTCAATCTTGAACTCATAGATTATTATCT 	721 ATTATCTCAATTTAGTTATTTATCTAGTGGGCCATTAAAAACTACCACATGTGTT 	181 TCTGTCTCCATTAGTCAATAACTAAACAAACGAGCAATTAGTAAGCCATGTGCCAGAT 	841 GCTCCGCTAGGCACCAGAGGATAAAACAATACTTATAGTATACCACTAATTTTCGCTT	901 AGTAACTAATGAAATGTTCAAGTCATGCCTCAAGAGTTGAGGAGACATTACAATGT 901 AGTAACTGATGAAATGTTCAAGTCATGCCTCAGTCAAGAGTTGAGGAGACATTACAATGT 901 AGTAACTGATGAAATGTCAAGTCATGCCTCAAGAGGTTGAGGAGACATTACAATGT	961 GTAATGGAAACCAAGGAAGTGAAACTTTGGATAAGTGGGGACTAGTGTATTTATATATT 	1021 TAATTGATTTCTGACTCTATCATTGGCCTCCAAACACAGATTGTGTTTTTCTTTGGTTTT

TTCCCATTCTGTTTGGATCTAT 1200 TATGCGCTTAAATTAAGATTAT 1260 ||||||||||||||||||||| TATGCGCTTAAATTAAGATTAT 1260 1740 AAGGGGATATCACCACCGATCC 2040 AATCTCCATCTCAAAATAATG 1380 AGGGTAAAGAAAGTGGGAGGA 1500 CCTGCACGACACACATAAAA 1980 GATTGTGTTTTTTTTTT 1080 TTTACTTAGCAGAACCACATAT 1620 |||||||||||||||||||||||||||| TTTACTTAGCAGAACCACATAT 1620 TGGCTTCAGGCTAAGAAGAAT 1800 TCAAACATTGGATTTTTCCTTA CACCTCTACGC 2088

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                                                      TGACCATGAAAGGTTCCTCAATGAAATGTTCCTCATTATCTTCAGAAGCCATATTATTCA
                                                                                                        CATTGACTTTGCAGTTAACTCCAGACCCTAGGTCTGGAATGCTGTCTTCTCTACTTATCCA
                                                                                                                         CATTGACTTTGCAGTTAACTCAGACCCTAGGTCTGGAATGCTGTCTTCTCTACTTATCCA
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                                                APPLICANT: An, Gang
APPLICANT: O'Hara, S. Mark
APPLICANT: Ralph, David
APPLICANT: Veltri, Robert
TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
TITLE OF INVENTION: MACGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
NUMBER OF SEQUENCES: 87
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                                                                                                                                                                                                                                                                                        COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,199
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REFERENCE/DOCKET NUMBER: UNC:018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 474-757
TELEPHONE: (512) 474-757
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 2505 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,787
FILING DATE: 31-UUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: NAKASHIMA, RICHARD
                                                                                                                                                                                            & Durkee
Sequence 85, Application US/09097199
Patent No. 6218529
GENERAL INFORMATION:
                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
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Best Local Similarity 99.4%;
Matches 1967; Conservative (
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STRANDEDNESS: single
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; LOCATION:
US-09-097-199-85
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Query Match
Best Local Similarity 99.1%;
Matches 1961; Conservative
                     ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15053
SEQ ID NO 15053
LENGTH: 6507
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Fatent No. 681239
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION WINDER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/237,768
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
FRIOR FILING DATE: 2000-09-08
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
ITILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PLILING DATE: 2000-10-20
PRIOR PLILING DATE: 2000-10-03
PRIOR PLILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PLILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: REALSEQ for Windows Version 4.0
SEQ ID NO 119365
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98.8%; Pred. No. 1.6e-132;
tive 1; Mismatches 4;
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Best Local Similarity 98.8%
Matches 596; Conservative
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RESULT 6 US-09-949-016-119366/c

RESULT 5 US-09-949-016-119365/c ', Sequence 119365, Application US/09949016

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US-09-949-016-119364/c
                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Human
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                                          APPLICATE: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 113466

LENGTH: 601
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98.8%; Pred. No. 1.6e-132;
tive 1; Mismatches 4;
Sequence 119366, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 98.8°
Matches 596; Conservative
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; ORGANISM: Human
US-09-949-016-119366
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RESULT

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FARCHIA NO. 9812339.

FARCHIA NO. 9812339.

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: 06/241,755

PRIOR FILING DATE: 2000-00-00

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PELICATION NUMBER: 66/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SSOFTWARE: FRATESEQ for Windows Version 4.0

LENGTH: 601
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Pred. No. 7.7e-76;
1; Mismatches 4; Indels 2;
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Patent No. 5882864
GENERAL INFORMATION:
APPLICANT: An, Gang
APPLICANT: C'Hard, S. Mark
APPLICANT: Ralph, David
TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
TITLE OF INVENTION: BIOMARKERS AND MANAGEMENT OF PROSTATE
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS:
DIAGRESSER: ARDOLG, White & Durkee
STREET: P.O. Box 4433
Sequence 119364, Application US/09949016
Patent No. 6812339
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98.1%;
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Best Local Similarity 98.1
Matches 368; Conservative
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US-09-949-016-119364
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US-09-097-199-3
Sequence 3, Application US/09097199
Sequence 3, Application US/09097199
Patent No. 6218529
GENERAL INFORMATION:
APPLICANT: An, Gang
APPLICANT: Ralph, David
APPLICANT: Ralph, David
APPLICANT: Weltri, Robert
ITILE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
ITILE OF INVENTION: BROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATCTGAAGAAACTTCCCAAGTGTAAGACTCTGCCTGCACGACAACACATAAA 1978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 96.2%; Pred. No. 1.1e-58;
Matches 282; Conservative 0; Mismatches 11; Indels
                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/692,787
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COTGLEY. Timochy S.
REGISTRATION NUMBER: 38,414
REFERENCE/POCKET NUMBER: UROC:012
TELERPHONE: (512) 418-3000
TELERPHONE: (512) 418-3000
TELERPHONE: (512) 414-7577
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
TENDERM: 757 base pairs
Texas
: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 757 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 77210
COMPUTER READABLE FORM:
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STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic
STRANDEDNESS:
  STATE: Te
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Sequence 1611. Application US/09949016

Sequence 1611. Application US/09949016

Sequence 1611. Application US/09949016

BENERAL INFORMATION:

APPLICANT: VBTTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WIMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-0-09

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 16151

TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1686 ACAACGACACATTCAGGAGTTAAATATTTTTCATCAAACATTGGATTTTTCCTTAACGCT 1745
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 13.2%; Score 275.4; DB 3; Best Local Similarity 96.2%; Pred. No. 1.1e-58; Matches 282; Conservative 0; Mismatches 11;
                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
APPLICATION DATA:
APPLICATION NUMBER: US 08/692,787
FILING DATE: 31-ULL-196
ATTORNEY/AGENT INFORMATION:
NAME: NAKABHIMA, RICHAR'A.
REGISTRATION NUMBER: P-42,023
REPERNEK/DOCKET NUMBER: URCC:018
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION TROUBLES:
INFORMATION FOR SEQ ID NO: 3:
EBNOTHENCE CHARACTER.STICS:
LENGTH: 757 base pairs
TYPE: NUCleic acid
TYPE: NUCleic acid
TYPE: NUCleic acid
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2085 ACGC 2088
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US-09-397-787-248/c
                                                                                                                                                                                                LENGTH: 573
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LENGTH: 430
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Fatent No. 681239

GENERAL INFORMATION:
FAPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TILLE OF INVENTION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR PELLING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
FRIOR FILING DATE: 2000-09-08
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 207012
SEQ ID NO 13733
                                                                                                                                                                                                                                                                138898 CAAAATTGATAGACCGCTAGCAAGACTAATAAAGAAAAAAGAGAGAAGAATCAAATAGAC 138957
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                                                                                                                                                   1943 CAAGTGTAAGACTCTGCCTGCACGACAACACATAAAAAAGAGAGAAGAAGAATCAAATAGAC 2002
                                                                                                                                                                                                                                       2003 ACAATAAAAATGATAAAGGGGATATCACCACCGATCCCACAGAAATACAAACTACCATC 2062
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                                                                 DB 4; Length 146401;
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                                                                                                          Indels
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Batent No. 6262334
GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCDNA-260XX
CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
                                                               Score 118.8; DB 4;
Pred. No. 7.3e-19;
0; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                    139018 AGAGAATACTACAAACACCTCTACGC 139043
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                                                           Query Match 5.7%;
Best Local Similarity 88.4%;
Matches 129; Conservative
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US-09-949-016-13733/c
    TYPE: DNA
ORGANISM: Human
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-385-982-420/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312 CAAGACTANATAAAAAAAGAGAGAAGAATCAAATAGACNCAATAAAAAATGATAAAGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Lodes, Michael J.
APPLICANT: Michael, Jennifer L.
APPLICANT: Michael, Jennifer L.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN:
TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS;
FILE REFERENCE: 210121.466C2
CURRENT APPLICATION NUMBER: US/09/397,787
CURRENT FILING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 334
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 115.6; DB 3
Pred. No. 5.1e-19;
0; Mismatches 6
EARLIER APPLICATION NUMBER: 09/328,111
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 248, Application US/09397787 Patent No. 6468758
                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)...(573)
; OTHER INFORMATION: n = A,T,C or G
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; OTHER INFORMATION: n = A,T,C or G
US-09-397-787-248
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Best Local Similarity 95.2%;
Matches 118; Conservative (
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US-09-245-2144/C

Sequence 44, Application US/09245281

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY

TITLE OF INVENTION: NOVEL MOSS THEREOF

FILE REFERENCE: 07334/11801

CURRENT FILING DATE: 1999-02-06

EARLIER PILING DATE: 1999-02-06

EARLIER PILING DATE: 1998-06-17

EARLIER PILING DATE: 1998-06-17

EARLIER PILING DATE: 1998-06-06

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PASESEQ for Windows Version 4.0

SEQ ID NO 44

LENGTH: 32042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.5%; Score 115.2; DB 4; Length 475; Best Local Similarity 97.5%; Pred. No. 5.9e-19; Matches 117; Conservative 0; Mismatches 3; Indels 0.
                                                                                                 APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Johert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET: 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILLING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 1218
LENGTH: 475
                      Sequence 12318, Application US/09621976 Patent No. 6639063 GENERAL INFORMATION:
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) ORGANISM: Homo sapiens
US-09-245-281-44
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ORGANISM: Homo sapiens
US-09-621-976-12318
US-09-621-976-12318/c
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Search completed: September 9, 2005, 06:27:38

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Sequence 143, Sequence 245,

US-11-057-807-143 US-10-278-698-245

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 US-09-974-546-33
 Sequence 3, Appl 1950

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 Sequence 420, App 115.2

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 Sequence 248, App 115.2

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 US-09-874-29-334
 Sequence 334, App 115.2

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 US-10-082-828A-143
 Sequence 143, App 142, App 142, App 142, App 142, App 142, App 142, App 143, App 1

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     ATTORNEY/AGENT INFORMATION:

NAME: Nakashima, Richard A.

REGISTRATION NUMBER: P-42,023

REFERENCE/DOCKET NUMBER: UROC:018

TELEPHONE: (512) 474-577

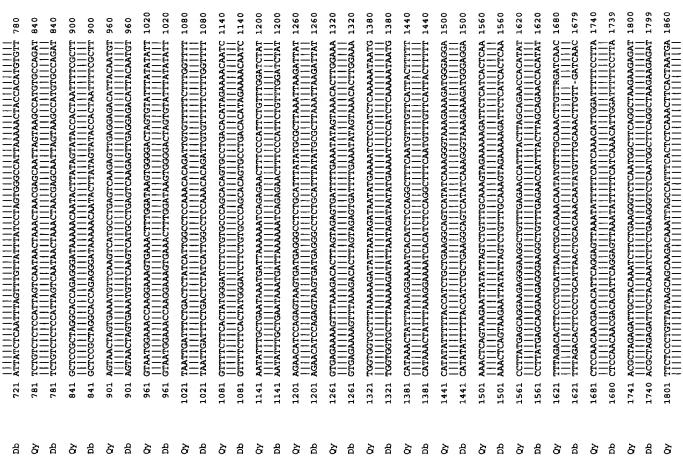
INFORMATION FOR SEQ ID NO: 83:

SEQUENCE CHARACTERISTICS:

LENGTH: 2087 base pairs

TYPE: nucleic acid

STRANDEDNESS: single
                                                                                                                                                        NAME/KEY: CDS
LOCATION: 99..503
SEQUENCE DESCRIPTION: SEQ ID NO: 83:
FILING DATE: 1998-06-12
                                                                                                                                      TOPOLOGY: linear
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BZ600251 V BZ604730 V AQ600990 I AQ355228 C BZ611286 V AG031791 I AW818026 C BX504526 I

Pan trogl CM3-ST027 DKFZp686M

WHABK34TF PM1-HT034 QV0-DT004 PM1-HT034 PM1-HT034

BZ600022 BQ358592 AW938273

AW938274 C BE154240 E AQ488905 F BQ353785 AV732317 A

ALIGNMENTS

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412 bp DNA linear GSS 14-APR-1999
RPCI11.34D16.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-34D16,
AQ045191
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1 (bases 1 to 412)
Adams, M.D., Rounaley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from thtp://www.tigr.org/tdb/humgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Class: BAC ends.
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/clone_lib="RPC1-11"
/noce="Vector: pPGA-63.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mark Addms
Contact: Mark Addms
Contact: Mark Addms
Department of Bukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Email: mdadms@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
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BE155549 PM2-HT035
AQ337692 HS_5017 A
AQ330351 RCL-BT031
BE154146 PM1-HT034
BE065326 RCL-BT031
BE154146 PM1-HT034
BE065400 RCL-BT031
BC05340 RCL-BT031
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              GenCore version 5.1.6
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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240 GATATCACCACCGATCCCACAGAAATACAAACTACCATCAGAGAATACTACAAACACCTC 181
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Context: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887

Fax: (206) 
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1 (bases 1 to 460)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Heller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
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                                                                                                                                                                                                                                                                                                              246 AAAGGGGATATCACCACCGATCCCACAGAAATACAAACTACCATCAGAGAATACTACAAA 187
                                                                                                                                                                                        306 GACTGCTAGAAGACTAATAAAAAAAGAGAAGAATCAAATAGACACAATAAAAAATGAT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ829037
HS_5023_B2_F06_SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic_clone Plate=599 Col=12 Row=L, genomic survey sequence.
                                                                                                                 1958 GCCTGCACGACACACATAAAAAAGAGAGAAGAATCAAATAGACACAATAAAAAATGAT
                                                                                                                                                                                                                                                               2018 AAAGGGGATATCACCACCGATCCCACAGAAATACAAACTACCATCAGAGAATACTACAAA
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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5.7%; Score 119; DB 8; Length 460;
Best Local Similarity 77.3%; Pred. No. 1e-15;
Matches 143; Conservative 0; Mismatches 42; Indels
                                               Indels
94.7%; Pred. No. 6.7e-16;
tive 0; Mismatches 7;
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/db_xref="taxon:9606"
/clone="Plate=599 Col=12 Row=L"
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Class: BAC sequence stop: 460.
High quality sequence stop: 460.
Location/Qualifiers
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GSS.
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Best Local Similarity 94.7%
Matches 124; Conservative
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JOURNAL MEDLINE PUBMED COMMENT

TITLE

PEATURES

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 6 arcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
BQ353836 150900-013-c12 HT0340 HRNA linear BST 20-MAY-2002
PM1-HT0340-150900-013-c12 HT0340 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMI&t2=PMI-HT0340-15090-013-c12&t3=2000-09-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 23
High quality sequence stop: 456.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Best Local Similarity
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OM protein

Run on:

Sequence:

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PAT 08-AUG-2001
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An,G., O'Hara,S.Mark., Ralph,D. and Veltri,R.
Biomarkers and targets for diagnosis, prognosis and management of prostate, breast and bladder cancer
Patent: US 621829-A 83 17-APR-2001;
Location/Qualifiers
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AF291612 F
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Sequence 83 from patent US 6218529.
AR146835.1 GI:15110024
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/organism="unknown"
/mol_type="unassigned DNA"
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Best Local Similarity:
Query Match:
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AR146835
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
     ORIGIN
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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/Cgn2_1/USPTO_epool/USO9974546/runat_07092005_174502_20945/app_query.fasta_1.654
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-DB=GenEmbl -QFYM=fastap -SUFFTX=p2n.rge -MINMATCH=0.1 -LCOPCL=0 -LCOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MINE 0 -ALIGN=15 -MODE=LOCAL
-UNFRY=ptc -NORM=ext -HEAPSIZE=550 -MINLEN=0 -MAXLEN=2000000000
-USER=US09974546_@CGN 1_1_2647_@runat_07092005_174502_20945 -NCPU=6 -ICPU=3
-NO MAAP -LARGEQDERS -NEG SCORES=0 -MAIT -DSPBEJCCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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AF189270 Homo sapi
BC069109 Homo sapi
AR146836 Sequence
                                                                                                                                                                 9, 2005, 13:07:44; Search time 2414 Seconds (without alignments) 2709.799 Million cell updates/sec
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                                                                                                                                                                                                                                                                US-09-974-546C-84
694
1 MRAFLRNQKYEDMHNIHIL.......TLGLECCLLYLSKTIHPQII 135
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                           version 5.1.6
- 2005 Compugen Ltd.
                                                                                                                      nucleic search, using frame plus p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4708233 segs, 24227607955 residues
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Maximum Match 100%
Listing first 45 summaries
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AF189270
BC069109
AR146836
                                                                                                                                                                                                                                                                                                                                                                                    Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                           GenCore
Copyright (c) 1993
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(bases 1 to 2103)

An. G. Meka, C.S., Luo, G., Bright, S.P., Cazares, L., Wright, G.L. Jr., and Veltri, R.W.
Cloning and characterization of UROC28, a novel gene overexpressed Cancer Res. 60 (24), 7014-7020 (2000)

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                                               99 ATGAGGCCTTCTTAAGGAACCAGAAATATGAGGATATGCACAATATTATTCACATTTTA 158
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An,G. and Veltri,R.W.
Direct Submission
Submitted (13-SEP-1999) UroSciences, UroCor, Inc., 840 Research
Parkway, Oklahoma City, OK 73104, USA
                           MetArgAlaPheLeuArgAsnGlnLysTyrGluAspMetHisAsnIleIleHisIleLeu
                                                                                          GlnIleArgLysLeuArgHisArgLeuSerAsnPheProArgLeuProGlyIleLeuAla
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mRNA, complete cds.
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US-09-974-546C-84 (1-135) x AR146835 (1-2087)
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AF189270
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/tissue_type="p;
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1 (bases 1 to 2496)

2 Strausberg, L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusinak, M. F., Bonaldo, M.F., Casavant, T.L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninoi, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McKenn, P.J., McKernan, K.J., Malek, J.A., Gardia, P.H., Richards, S., Wolley, K.C., Halles, S., Gardia, P.H., Richards, S., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
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HOMO Sapiens prostate and breast cancer overexpressed 1, mRNA (cDNA clone IMAGE:7216926).
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Conservative:
Mismatches:
Indels:
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/gene="UC28"
/note="alternative splicing"
2047. .2052
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       396 TCTTCAGAAGCCATATTATTCACATTGACTTTGCAGTTAACTCAGACCCTAGGTCTGGAA 455
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An,G., O'Hara,S.Mark., Ralph,D. and Veltri,R.
Biomarkers and targets for diagnosis, prognosis and
prostate, breast and bladder cancer
Patent: US 6218529-A 85 17-APR-2001;
Location/Qualifiers
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/wol_type="unassigned DNA"
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Series: Plate: Row: Column: 0.
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Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnorch,A., Schlein,J.B., Jones,S.J. and Marra,M.A. Generation and initial analysis of more than 15,000 full-length Muman and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
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                                                                                                                                                                                          Submitted (16-APR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                                                                                                             Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Anup Madan, University of Iowa
CDNA Library Preparation: Anup Madan, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Neurogenomics Research Lab,
200 B EMRB, University of Iowa, Iowa City, IA-52242
anup-madan@ulowa.edu
Jessica Fahey, Tim Nelson, Jae Goon Yoon and Anup Madan
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Matches:
Conservative:
Mismatches:
Indels:
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/tissue type="Synthetic c/clone lib="NIH MGC_242"
/lab host="XL10"
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/db_xref="taxon:9606"
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Direct Submission
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AUTHORS
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KEYWORDS
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LLPFCYKVFRKKEKVKRSQKATEFIDYSIEQSHHAILTPLQTHLTMKGSSMKCSSLSS
EAILFTLTLQLTQTLGLECCLLYLSKTIHPQII"
          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Butheria, Primates; Catarrhini, Hominidae, Homo.

1 (Dasas 1 to 2512)

An, G., Ng, A.Y., Meka, C.S., Luo, G., Bright, S.P., Cazares, L., Wright, G.L. Jr. and Veltri, R.W.

Cloning and characterization of UROC28, a novel gene overexpressed th prostate, breast, and bladder cancers

Cancer Res. 60 (24), 7014-7020 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219 CCAGAAACTGTGCTCTTACCATTCTGCTACAAGGTATTTCGAAAAAAGAAAAAGTAAAA 278
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                                                                                                                                                                               2 (bases 1 to 2512)
An,G. and Veltri,R.W.
Direct Submission
Submitted (23-SEP-1999) UroSciences, UroCor, Inc., 840 Research
Parkway, Oklahoma City, OK 73104, USA
Location/Qualifiers
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protein_id="AAG17117.1"
db_xref="G1:10441602"
                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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/gene="UC28"
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/gene="UC28"
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Homo sapiens
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                                                NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                         4769: contig of 4769 bp in length
4869: gap of unknown length
11657: contig of 6788 bp in length
11757: gap of unknown length
28189: contig of 16432 bp in length
53341: contig of 25052 bp in length
53441: gap of unknown length
102327: contig of 48886 bp in length
102427: gap of unknown length
Quality coverage: 5.84 in Q20 bases; agarose-fp
Quality coverage: 5.57 in Q20 bases; sum-of-contigs
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gap of unknown length
contig of 80354 bp in length
gap of unknown length
contig of 3817 bp in length.
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/note="assembly_name:Contig12"

/note="assembly_name:Contig12"

28290. .53341

/note="assembly_name:Contig13"

6347. .102337
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/db_xref="taxon:9606"
/chromosome="6"
/clone="RP11-133015"
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No
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                                                                                                    29892 ATGAGGGCCTTCTTAAGGAACCAGAAATATGAGGATATGCACAATATTATTGACATTTTA 29951
                                                                                                                                                                         ACUACASE 186698 bp DNA linear HTG 01-SEP-2000 Homo sapiens chromosome 6 clone RP11-133015, WORKING DRAFT SEQUENCE, 7 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30192 refreadadecentarrenearreactreactrecerraacreagacerragereregaa 30251
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Submitted (07-APR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Sep 1, 2000 this sequence version replaced gi:7523932.
                                                                                                                                                                                                                                                                                                                                                                                       LeuThrProLeuGlnThrHisLeuThrMetLygGlySerSerMetLygCysSerSerLeu 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerSerGluAlaIleLeuPheThrLeuThrLeuGlnLeuThrGlnThrLeuGlyLeuGlu 120
                                                                                                                                                                                                                            41 ProGluThrValLeuLeuProPheCysTyrLysValPheArgLysLysGluLysValLys 60
                                                                                                                                                     40
                                                                                                                                                                                                                                                                                                            80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                          61 ArgSerGlnLysAlaThrGluPhelleAspTyrSerIleGluGlnSerHisHisAlaIle
                                                                                                                                                 21 GlnileArgiysLeuArgHisArgLeuSerAsnPheProArgLeuProGlyIleLeuAla
                                                                        MetArgAlaPheLeuArgAsnGlnLysTyrGluAspMetHisAsnIleIleHisIleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30252 TGCTGTCTTCTCTATCCAAAACTATACATCACAGATCATA 30296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 CysCysLeuLeuTyrLeuSerLysThrlleHisProGln1leIle 135
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                                  US-09-974-546C-84 (1-135) x HS171N11 (1-129227)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence of Homo sapiens clone Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACO36236.2 GI:9958166
HTG: HTGS_PRASE1; HTGS_DRAFT.
HOMO sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 186698)
Waterston, R.H.
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(bases 1 to 259920)
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                                                                                                                      Direct Submission
Unpublished
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Direct Submission
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SMANTAD. MARTEL. METZEL, M. LEE., ADMIN. B., ANDHIANO, D., Allen, H., Alsbrocks, S., Amin. A., Anguiano, D., Allen, H., Alsbrocks, S., Amin. A., Anguiano, D., Angalabechi, V., Alsbrocks, S., Amin. A., Anguiano, D., Angalabechi, V., Alsbrocks, S., Amin. A., Anguiano, D., Bandaranike, D., Barber, M., Barnstead, M., Benahmed, F., Baldin, D., Bandaranike, D., Barber, M., By The, P., Canderon, E., Carderon, E., Carderon, E., Carderon, E., Char, Z., Chan, Y., Martin, Y., Machan, Y., Martin, Y., 
                                                        159552 TCTTCAGAAGCCATATTATTCACATTGACTTTGCAGTTAACTCAGACCCTAGGTCTGGAA 159611
159432 AGAAGTCAAAAGGCAACAGAGTTCATTGATTATTCCATAGAACAGTCACACACCATGCAATT 159491
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACUSES 259920 bp DNA linear HTG 10-MAY-2003 Rattus norvegicus clone CH230-18J15, WORKING DRAFT SEQUENCE, 2 UNDOCASTE DISCES.
                                                                                                                                                                              SerSerGluAlaileLeuPheThrLeuThrLeuGlnLeuThrGlnThrLeuGlyLeuGlu 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                         159612 TGCTGTCTTCTTACTTATCCAAACTATACATCCACAGATCATA 159656
                                                                                                                                                                                                                                                                                                    CysCysLeuLeuTyrLeuSerLysThrlleHisProGlnIlelle 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC096345.6 GI:30521870
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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AC096345/c
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Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Daylor Plaza, Houston, TX 77030, USA

On May 10, 2003 this sequence version replaced gi:24818617.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.red/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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NOTE: This sequence may represent more than one clone.

NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces arbitrary. Gaps between the corder in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                   Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Paylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 259920).

Rat Genome Sequencing Consortium.
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Consensus quality: 240867 bases at least Q40
Consensus quality: 244203 bases at least Q30
Estimated insert size: 252807; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Baylor College of Medicine
Center code: BCM

    .259920
    /organism="Rattus norvegicus"

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1. 1739
1. 1739
1. 4048= and extension clone_end: 77"
8054. 8862
/note="Clone_boundary
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Center clone name: CH230-18J15
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/db_xref="taxon:10116"
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on human chromosome 22 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (21), 11354-11358 (2000) PUBMED 11005839 REFERENCE 2 (bases 1 to 9833) TITLE Direct Submission P. Trexler, Pu,YX., Ramsay,M., Jenkins,T., Leskinen,E., Pamilo,P., Trexler,M., Patthy,L., Jorde,LB., Yu,N. and Li,WH. JOURNAL Submitted (01-AUG-2000) Human Genetics Center, University of Texas at Houston Health Science Center, 6901 Bertner Ave., Houston, TX TO30, USA FEATURES 1. 1983 Acadisman Acadism	ignment Scores: ed. No.: ore: ore: scent Similarity: 34.10\$ Con st Local Similarity: 24.28\$ ind ery Match: -09-974-546C-84 (1-135) x AF291597 (1-98 4 PheLeuArgAsnGlnLysTyrGluAspM	19	Qy 104 AlaIle
misc_feature com_lement(248170249015) misc_feature com_lement(248170249015) Clone end:Sp6 site:Ecori end sequence:BH360925 Clone end:Sp6 site:Ecori 249451251486 /note="wag=end-extension clone end:Sp6" /note="wag=end-extension clone end:S	10 TyrGluAspWetHisAsnIleIleHisIleLeuGlnIleArgLysLeuArgHisArgLeu 10 TyrGluAspWetHisAsnIleIleHisIleLeuGlnIleArgLysLeuArgHisArgLeu 1::	195290 TTCCTGCCTTCTGTTTCAAATCTTTTGGAAAGAACTGAGTAGGTGGATAAAATATCA 1 61 ArgSerGlnLysalaThrGluPheIleAspTyrSerIleGluGluGlaStHisHis 7	Qy 119 LeuGluCysCysLeuLeuTyrLeu 126 Db 195098 TTACAGAAGTGCTTAGCATATCTT 195075 RESULT 9 AP291597 LOCUS AP291597 LOCUS AP291597 AP291597 LOCUS ACCESSION AF291597 AF291597 AF291597 ACCESSION AF291597 AF2

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                              3279 AAAATGGAACCACATGGTCTGTTCCTGAATTCTCCAACAGATCCCTTTGGTCCCAACCTC 3338
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Pamilo, P., Trexler, M., Patthy, L., Jorde, L.B., Yu, N. and Li, W.-H.
Worldwide DNA sequence variation in a 10-kilobase noncoding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (01-AUG-2000) Human Genetics Center, University of Texas at Houston Health Science Center, 6901 Bertner Ave., Houston, TX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 LeuGlnThrHisLeuThrMetLysGlySerSerMetLysCysSerSerLeuSerSerGlu 103
                                                                                                                                                                                                                     Horizon 19817 bp DNA linear PRI 24-OCT-200 Memo sapiens isolate South African MeJe 22q11.2 noncoding genomic AF291631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 9817)

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Zhao,Z., Jin,L., Fu,Y.-X., Ramsay,M., Jenkins,T., Leskinen,E.,
Pamilo,P., Trexler,M., Patthy,L., Jorde,L.B., Yu,N. and Li,W.-H.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on human chromosome 22
Proc. Natl. Acad. Sci. U.S.A. 97 (21), 11354-11358 (2000)
20481912
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42
17
38
36
76
                                                                                                                  3339 CAAGTGAGGCTCATTTATTCTCTCTAGCTCTACACCCT 3377
                                                                                       120 GluCysCysLeuLeuTyrLeuSerLysThrIleHisPro 132
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Matches:
Conservative:
Mismatches:
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/mol type="genomic DNA"
/mol type="genomic DNA"
/isoTarte="South African MeJe"
/db_xref="taxon:9606"
/chromosome="22"
/map="22q11.2"
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/note="noncoding region"
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1 (Dases 1 to 9432)

Zhao, Z., Jin, L., Fu, Y. -X., Ramsay, M., Jenkins, T., Leskinen, E., Manilo, P., Treakler, M., Patthy, L., Jorde, L.B., Yu, N. and Li, W.-H. Worldwide DNA sequence variation in a 10-kilobase noncoding region on human chromosome 22
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Zhao, Z., Jin, L., Fu, Y.-X., Ramsay, M., Jenkins, T., Leskinen, E.,
Pamilo, P., Trexler, M., Patthy, L., Jorde, L.B., Yu, N. and Li, W.-H.
Direct Submission
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Db 3083 TTAACTACACCCTTTACTGCCTCCAAAATTATGCTGAATGCTCTGATATCCTGTCAGGA 3142	Oy 104 Alaile109 Oy 104 Alaile	Db 3143 GATATTTTCTCTAATAAAATAGGGATGGGAGGTGTGTTGGGGGGAGCTTTCTAGCTTG 3202	<pre>Qy 110 ThrLeuGlnLeuThrGlnThrLeuGly</pre>	OY 119Leu 119 13263 AAAATGGAACCACATGGTCTGTTCCTGAATTCTCCAACAGATCCCTTTGGTCCCAACCTC 3322	Qy 120 GluCysCysLeuLeuTyrLeuSerLysThrIleHisPro 132 ::: bb 3323 CAAGTGAGGCTCATTTTATTCTCTCACACCCT 3361	RESULT 12 AF291632 LOCUS DEFINITION Homo sapiens isolate South African Kung 22q11.2 noncoding genomic aCCESSION AF291632 VERSION AF291632.1 GI:10953234	ALTIWORUS . ORGANISM Homo sapiens (human) ORGANISM Homo sapiens District Metaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia: Butheria: Primates: Catarrhin: Hominidae, Homo		MEDLINE 20481912 PUBMED 11005839 REFERENCE 2 (bases 1 to 9817) AUTHORS Zhao,Z., Jin,L., Fu,YX., Ramsay,M., Jenkins,T., Leskinen,E., Pamilo P. Trezler M. Patthy, I. Jorde I. B. Y., N. and I.i M. H	TITLE Direct Submission JOURNAL Submission JOURNAL Submisted (01-AUG-2000) Human Genetics Center, University of Texas at Houston Health Science Center, 6901 Bertner Ave., Houston, TX 77030, USA	FEATURES Location/Qualifiers 1. 9817 Organism="Homo sapiens" Corganism="Homo sapiens" Corganism="Homo sapiens" Corganism="Homo sapiens" Corganism Sapiens" Corganism Sapiens Corganism Sapiens	/holate="Sound: African Kung" /db_xref="taxon:9606" /chromosome="22"	misc_feature /maps=22q11.2" 1. 9817 note="noncoding region"	GOOFES:	ed. No.: 10.4 zre: 94.00 rcent Similarity: 34.10\$ str Local Similarity: 24.28\$ sry Match: 13.54\$	Gaps: x AF291632 (1-9817)	Qy 4 PheLeuArgAenGlnLysTyrGluAspWetHisAsnileIleHisIleLeuGlnIleArg 23	24 LysLeuArgHisArgLeuSerAsnPheProArgLeuProGlyIleLeuAlaProGluThr

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Zhao,Z., Jin,L., Fu,Y.-X., Ramsay,M., Jenkins,T., Leskinen,E., Pamilo,P., Treakler,M., Patthy,L., Jorde,L.B., Yu,N. and Li,W.-H.
Worldwide DNA sequence variation in a 10-kilobase noncoding region human chromosome 22
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Zhao, Z., Jin, L., Fu, Y.-X., Ramsay, M., Jenkins, T., Leskinen, E.,
Pamilo, P., Trexler, M., Patthy, L., Jorde, L.B., Yu, N. and Li, W.-H.
Direct Submission
Submitted (01-AUG-2000) Human Genetics Center, University of Texas at Houston Health Science Center, 6901 Bertner Ave., Houston, TX
77030, USA
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Homo sapiens isolate Chinese 1 22q11.2 noncoding genomic sequence.
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Homo sapiens isolate Chinese 2 22q11.2 noncoding genomic sequence.
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1 (Bases 1 to 983)

Zhao, Z., Jin, L., Fu, Y. - X., Ramsay, M., Jenkins, T., Leskinen, E., Manilo, P., Trexkler, M., Patthy, L., Jorde, L.B., Yu, N. and Li, W.-H. Worldwide DNA sequence variation in a 10-kilobase noncoding region human chromosome 22
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Zhao, Z., Jin, L., Fu, Y.-X., Ramsay, M., Jenkins, T., Leskinen, E., Pamilo, P., Trexler, M., Patthy, L., Jorde, L.B., Yu, N. and Li, W.-H. Direct Submission
Submitted (01-AUG-2000) Human Genetics Center, University of Texas at Houston Health Science Center, 6901 Bertner Ave., Houston, TX 77030, USA
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/isolate="Chinese 2"
/db_xref="taxon:9606"
/chromosome="22"
/map="22q11.2"
1. 9833
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/product= "Prostate cancer marker protein"
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-Q=/cgn2_1/USPTO_spool/US09974546/runat_07092005_174501_20885/app_query.fasta_1.654
-DB=N_Geneseq_16Dec04_-QFMT=fastap_-SUFFIX=p2n.rng -MINMATCH=0.1_-LOOPEXL=0
-LOOPEXT=0 -UNITS=bits -STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORES=pct -THR MAX=100 -TRR MIND=0 -ALIGN=15
-MODB=LOCAL. -OUTFMT=pto -NORM=ext -HRAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09974546_@CGN 1 1 468_@runat_07092005_174501_20885 -NCPU=6 -ICPU=3
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Nucleic acid marker; biomarker; tumour; prostate cancer; bladder cancer; benign prostatic hyperplasia; BPH; breast cancer; human; immunodetection; diagnosis; PCR primer; 88.

Prostate disease marker UC Band #28.

19-APR-2000 (first entry)

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The sequence represents nucleic acid biomarker UC band 28 #2, used in detection of prostate, breast and bladder cancer. Biomarker nucleic acid sequences can be used as hybridisation probes and primers that specifically hybridise to prostate cancer. benign prostatic hyperplasia (BPH), bladder cancer or breast cancer markers. Proteins encoded by the nucleic acid markers can be used to produce antibodies for the detection of prostate, breast or bladder cancer. The nucleic acids can be used as targets for therapeutic intervention in these diseases, in the identification and isolation of full-length gene sequences, including regulatory elements for gene expression, from genomic human DNA libraries, as hybridisation probes for screening genomic human DNA libraries. The kits comprising the nucleic acid sequences are useful for detecting bladder, breast or prostate cancer cells in a biological sample
                                                                                                                                                                                         New nucleic acids as biomarkers and targets useful for detecting, diagnosing, prognosing, and in developing treatments for prostate, breast and bladder cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2087 BP; 740 A; 406 C; 337 G; 604 T; 0 U; 0 Other;
                                                                      An G, O'hara SM, Ralph D, Veltri R;
                                                                                                                                                                                                                                                                                        Claim 2; Col 117-121; 78pp; English.
                                                                                                                   WPI; 2001-289849/30
P-PSDB; AAU02174.
                         (UROC-) UROCOR INC
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99WO-US013151.

11-JUN-1999;

16-DEC-1999

Homo sapiens WO9964631-A1

> 2087 135 0 0 0 Length:
> Matches:
> Conservative:
> Mismatches:
> Indels: 2.6e-76 694.00 100.00% 100.00%

159 CAGATCAGAAAATTGAGGCACAGATTAAGTAACTTCCCAAGGCTACCAGGCATTCTAGCT 218 LeuThrProLeuGlnThrHisLeuThrMetLysGlySerSerMetLysGysSerSerLeu 100 CTCACACCCTTGCAGACACACTTGACCATGAAAGGTTCCTCAATGAAATGTTCCTCATTA 398 101 SerSerGluAlaIleLeuPheThrLeuThrLeuGlnLeuThrGlnThrLeuGlyLeuGlu 120 GINI1eArgLysLeuArgHisArgLeuSerAsnPheProArgLeuProGly11eLeuAla 40 1 MetArgAlaPheLeuArgAsnGlnLysTyrGluAspMetHisAsnIleIleHisIleLeu 20 ProGluThrValLeuLeuProPheCysTyrLysValPheArgLysLysGluLysValLys ArgSerGlnLysAlaThrGluPheIleAspTyrSerIleGluGlnSerHisHisAlaIle US-09-974-546C-84 (1-135) x AAS04000 (1-2087) Percent Similarity: Best Local Similarity: Alignment Scores: 81 339 41 61 Query Match: DB: 셤 ð 셤 ठे 셤 ò 유 ઠે 요 ò

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The invention provides nucleic acid markers of prostate, breast and bladder cancer. The markers are indicators of malignant transformation of prostate, breast and bladder tissues and are diagnostic of the potential also be used as targets for the repetit to the prostate cancer. The nucleic acid can also be used targets for therapeutic intervention in prostate cancer. The markers may be used to design specific probes and primers, for the rapid analysis of prostate, bladder or breast tancer. The primers may also be used for in situ hybridization or in situ PCR detection and diagnosis. They may also be used to identify and isolate full length gene sequences form various DNA libraries. Antibodies against the polypeptide products of the markers can be used to treat prostate to ancer, bladder cancer or breast cancer. The encoded proteins may be used to detect antibodies. The proteins and antibodies can be used in immunodetection methods for detecting or quantifying the cancers, and for clinical diagnosis of these cancers. The antibodies may also be used for calinical diagnosis of these cancers. The antibodies may also be used for calinical diagnosis of these cancers. The antibodies may also be used for calinical diagnosis of these cancers. The antibodies may also be used for calinical diagnosis of these cancers. The antibodies may also be used for calinical diagnosis of these cancers. The antibodies may also be used for calinical diagnosis of these cancers. 218 Novel RNA biomarkers for diagnosis, prognosis and management of prostate, 20 21 GlnIleArgLysLeuArgHisArgLeuSerAsnPheProArgLeuProGlyIleLeuAla 40 ProGluThrValLeuLeuProPheCysTyrLysValPheArgLysLysGluLysValLys 60 CAGATCAGAAAATTGAGGCACAGATTAAGTAACTTCCCCAAGGCTACCAGGCATCTAGCT 1 MetArgAlaPheLeuArgAsnGlnLysTyrGluAspMetHisAsnIleIleHisIleLeu Sequence 2088 BP; 740 A; 406 C; 337 G; 604 T; 0 U; 1 Other; radioimaging to quantify and localize the encoded proteins Length: Matches: Conservative: Mismatches: Indels: US-09-974-546C-84 (1-135) x AAZ87583 (1-2088) Veltri RW; Claim 1; Page 182-183; 191pp; English 98US-00097199 O'hara SM, Ralph D, 2.6e-76 694.00 100.00% 100.00% breast and bladder cancer. 2000-116557/10. (UROC-) UROCOR INC Percent Similarity: Best Local Similarity: P-PSDB; AAY59295 12-JUN-1998; Alignment Scores: 41 Query Match: An G, ð d à g ð

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CysCysLeuLeuTyrLeuSerLysThrlleHisProGlnllelle 135 TGCTGTCTTCTCTATCCAAAACTATACATCCACAGATCATA

121 459

ò g AAZ87583 standard; DNA; 2088 BP

AAZ87583

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BP; 822 A; 519 C; 446 G; 718 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acids as biomarkers and targets useful for detecting, prognosing, and in developing treatments for prostate, breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   libraries. The kits comprising the nucleic acts between the biological sample detecting bladder, breast or prostate cancer cells in a biological sample
                 CTCACACCCTTGCAGACACACTTGACCATGAAAGGTTCCTCAATGAAATGTTCCTCATTA 398
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ArgSerGlnLysAlaThrGluPheIleAspTyrSerIleGluGlnSerHisHisAlaIle
                                                                                                                                                                                                                                                                                 Biomarker UC band 28 #3, used in diagnosis and prognosis of cancer.
                                                                                                                                                                                                                                                                                                        Prostate; breast, bladder; cancer; biomarker; probe; diagnostic;
benign prostatic hyperplasia; BPH; therapeutic; human; ss.
                                                                                                                                         CysCysLeuLeuTyrLeuSerLysThrIleHisProGlnIleIle 135
                                                                                                                                                      /product= "Prostate cancer marker protein"
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P-PSDB; AAU02175.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acids
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11-JAN-1996;
31-JUL-1996;
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and bladder
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LeuThrProLeuGlnThrHisLeuThrMetLysGlySerSerMetLysCysSerSerLeu 100
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                                                                                                                                                                                                  MetArgAlaPheLeuArgAsnGlnLysTyrGluAspMetHisAsnIleIleHisIleLeu
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                                             Conservative:
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3.39e-76
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P-PSDB; AAY59296.
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                                         Percent Similarity:
Best Local Similarity:
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pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polynucleotide; gene; ss.

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The invention provides nucleic acid markers of prostate, breast and bladder cancer. The markers are indicators of malignant transformation of prostate, breast and bladder tissues and are diagnostic of the potential for metastatic spread of malignant prostate tumours. The nucleic acid can also be used as targets for therapeutic intervention in prostate cancer, benign prostatic hyperplasia (BPH), bladder cancer or breast cancer. The markers may be used to design specific probes and primers, for the rapid primers may also be used for in situ hybridization or in situ PCR detection and diagnosis. They may also be used to identify and isolate fill length gene sequences form various DNA libraries. Antibodies against the polypeptide products of the markers can be used to treat prostate cancer, bladder cancer or breast cancer. The encoded proteins may be used to detect antibodies. The proteins and antibodies can be used in immunodetection methods for defecting or quantifying the cancers, and for immunodetection methods for defecting or quantifying the cancers, and for calinical diagnosis of these cancers. The encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2506 BP; 822 A; 519 C; 446 G; 718 T; 0 U; 1 Other;
                               Claim 1; Page 184-186; 191pp; English.
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20-FEB-2003; 2003US-00369493. 21-FEB-2002; 2002US-0360039P

US2003233675-A1

Bacteria.

CAO Y. HINKLE G J. SLATER S C. CHEN X.

(CHEN/)

CAOY/) (HINK/)

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Alignment Scores:
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Recombinant DNA construct, transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;

Bacterial polynucleotide #20398

02-DEC-2004 (first entry)

ADT45647 standard; cDNA; 1113 BP

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypoptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant to such as maize or soybean. The method of producing a transformed plant with the crecombinant DNA construct and growing the transformed plant with the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plants with the polynucleotide or polypeptide is useful for improving plants with the comprant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the content, improved plant growth and development under at least one stress condition, improved lignin production of carbohydrate, introgen or phosphorus use and/or uptake, by modification of photosynthesis or by production. This sequence represents a bacterial polynucleotide used in the scope of the invention. Note: The sequence data for this patent did content from part of the printed specification but was obtained in electronic form part of the parinted specification but was obtained in electronic form part of the patinted specification but was obtained in electronic format from USPTO at sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
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                                                                                                      327
                                                                                                                                                                                                115 ACAAACÁÁCAGGCÓACGGGAAAGGAAGAAGAGCTTAAGAGATATGGAATAGAGCTCATA 174
                                                                                                                                                                                 93 SerSerMet---LysCysSerSerLeuSerSerGluAlaIleLeuPheThrLeuThrLeu 111
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                                            53
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                                                                                                                                                                                                                                                                                                                                                                                          Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomanna; bacterial polymucleotide; gene; se.
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                                                                                                                                    73 IleGluGlnSerHisHisAlaIleLeuThrProLeuGlnThrHisLeuThrMetLysGly
                                                                                                                                                       271 ATAATTCATTCTCATGCA---TTCACACCTCTCTCTTAAAAGGCTTTAAAAAGCTGGG
                                           34 ArgleuProGlyIleLeuAlaProGluThrValLeuLeuProPheCysTyrLysValPhe
                                                                                      54 ArglyslysglulysVallysArgSerGlnLysAlaThrGluPhelle---AspTyrSer
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                                                        Bacterial polynucleotide #1334
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HINKLE G J.
SLATER S C.
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(GOLD/)
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transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transformed a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant with the polynucleotide or polypeptide is useful for producing plant properties.

The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan the secope of the invention. Note: The sequence data for this patent did content form part of the printed specification but was obtained in electronic format from USPTO at sequence. The sequence was obtained in electronic format from USPTO at sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||||||||||:::
70 ATGCACAACTTA-----GCCATAAAGCTGAGAGAAAGAGGGGATGAAGTGGGAATAGTC 123
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                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerSerLeuSerSerGluAlalleLeuPheThrLeuThrLeuGlnLeuThrGlnThrLeu 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 HisIleLeuGlnIleArgLysLeuArgHisArgLeuSerAsnPheProArgLeuProGly 37
                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 LysValLysArgSerGlnLysAlaThrGluPhelleAspTyrSerIleGluGlnSerHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 HisAlalleLeuThrProLeuGlnThrHisLeuThrMetLysGlySerSerMetLysCys
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                                                                                                                                                                                                          Claim 1; SEQ ID NO 34867; 21pp + Sequence Listing; English.
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                                                                            23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                         23-MAR-2001; 2001WO-US009231
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Drosophila melanogaster
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8 8 8

30 SerAsnPheProArgLeuProGlyIleLeuAlaProGluThrValLeuLeuProPheCys 49

causing an amino

of the PLCG1 gene (reference sequence GI 11345540)

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Diagnosing and prognosing vascular disease, e.g. coronary artery disease and myocardial infarction, based on the detection of polymorphisms in the phospholipase C gamma 1 and plasminogen activator inhibitor type 2 genes and polypeptides.
385 TATAACTTACCCAATCTAGTTTGGGTTTGGCTTCCACAGGAACA------TGT 338
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                                                                                                                                                                                                            SerLeu-----SerSerGluAlalleLeuPheThrLeuThrLeuGlnLeuThrGln 115
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                                                                                            69 -----IleAspTyrSerIleGluGlnSerHisHisAla-----IleLeuThr---
                                                                                                                       277 GITITIGICADAACTITICAGCADCICCACTGCAAACGCIGCAGAIGIGCIGACCGGC
                                                                                                                                                   83 ------ProLeuGlnThrHisLeuThrMetLysGlySerSerMetLysCysSer
                                     50 TyrLysValPheArgLysLysGluLysValLysArgSerGlnLysAlaThrGluPhe---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human; single nucleotide polymorphism; SNP; phospholipase C gamma 1; PLGZI; gene; vascular disease; plasminogen activator inhibitor type 2 PAI-2; diagnosis; atherosclerosis; coronary artery disease; ischemia; myocardial infarction; stroke; thromboembolism; de.
                                                                                                                                                                                                                                                                   116 ThrieuGlyLeuGluCysCys-----LeuLeuTyrLeuSer 127
                                                                                                                                                                                                                                                                                              115 TCTCTTGCTACACAGTGTTGTTCTGCGCTGATTCTCTGCTTATCA 71
                                                                                                                                                                                                                           157 TCTACTCTCTGACTCCTCACATGCTATCATGTTCACTATG-
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28-AUG-2001; 2001US-0315572P.
05-OCT-2001; 2001US-0327488P.
14-DEC-2001; 2001US-00017128.
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The invention relates to methods, agents and apparatus for diagnosing and prognosing vascular diseases based on the detection of polymorphisms in the phospholipase C gamma 1 (PLGGI) and plasminogen activator inhibitor type 2 (PAI-2) genes and polypeptides. In a preferred claim of the invention the polymorphism is a C to T nucleotide change at position

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29020 ATTATCCCCATTTTCCAGATGAAAAACTGAGGCACAGAGCTAAAAGGCAGGATTCAAAC 28961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus facealis genome. AAX13919 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences. Also known as contigs. The computer-based system can identify fragments of the Enterococcus facealis genome with commercial importance. The products can be used to detect the presence of Enterococcus facealis in samples. They can also be used for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus infection.
       acid change from Threatone to Isoleucine at position 813 of the protein. This sequence represents the region of the PLCG1 gene with the T form of the polymorphism. The methods, agents and apparatus is used for diagnosiming and prognosimal vaccular diseases e.g. atherosclerosis, coronary artery disease (especially), myocardial infarction (especially), ischemia, stroke, peripheral vascular diseases, venous thromboembolism and pulmonary embolism
                                                                                                                                                                                                                                                                                                                                                                      16 IlelleHislleLeuGlnIleArgLysLeuArgHisArgLeuSerAsnPheProArgLeu 35
                                                                                                                                                         G; 41031 T; 0 U; 0 Other;
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Conservative:
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97US-0046655P.
97US-0066009P.
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Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nuclectide sequences can be used in vaccines to prevent or attenuate an Enterococcal infection
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                                                                                                                               readable medium having recorded on it a Enterococcus faecalis
le sequence useful for detecting diseases related to Enterococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated cancer-associated polynucleotides and polypeptides useful for diagnosing, preventing or treating cancers, especially lymphoma and leukemia, or in screening for agents that modulate cancer.
                                                                                                               Mouse; ds; cancer-associated protein; gene; cytostatic; cancer;
leukaemla; lymphoma; CAP.
                                                                                Mouse cancer-associated genomic DNA MD13-011
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15-APR-2003; 2003US-00417375.
13-JUN-2003; 2003US-00461862.
                                                                                                                                                                                                                                                                                                                                                                                                                           15-SEP-2003; 2003US-00663431.
                                                                                                                                                                                                                                                                                                    17-FEB-2004; 2004WO-US004730.
                                                                                                                                                                                                                                                                                                                                               14-FEB-2003; 2003US-00367094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SAGR-) SAGRES DISCOVERY INC
                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-652914/63.
                                                                                                                                                                                                                         WO2004074320-A2
                                                                                                                                                                                   Mus musculus.
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Pred. No.:
                                        18-NOV-2004
                                                                                                                                                                                                                                                                 12-SEP-2004
ABD32622;
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Length:

6.32e+03

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9899
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                                                                                                                                                                                                                                                                                ------CAA 9812
                                                                                                                                                                                                                                                                                                                                                 9811 TTTİCCİCTAAAGGAAACAGTTTTAAACTATATAAATATTGCTCCİİTTİAATATCTTT 9752
                                                                                                                                                                                                                                                                                                                 97 CysSerSerLeuSerSerGlu-------AlaIleLeuPheThrLeuThr 110
                                                                                                                                                                          16
                                  17 IleHisIleLeuGlnIleArgLysLeuArgHisArgLeuSerAsnPheProArgLeuPro 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovine, 88; BST; expressed sequence tag; lactation; LMFD;
muscle deposition; fat deposition; genome mapping; gene identification;
gene analysis; cattle breeding.
                                                        :::||| ||| :::
9988 CTACATGCACTGCTAAATGGTGATGTCAGATTTGGTTTTACTAACTTCTCCAAA-----
                                                                                                                           57 GluLysValLysArgSerGlnLysAlaThrGluPhelleAspTyrSerIleGluGlnSer
                                                                                                                                                                                                                                                                                                                                                                                    111 LeuGlnLeuThrGlnThrLeuGlyLeuGluCysCysLeuLeuTyrLeuSerLysThrile
                                                                                                     37 GlyIleLeuAlaProGluThrValLeuLeuProPheCysTyrLysValPheArgLysLys
                                                                                                                                                                                                         9898 AAAAAAAAAAAGGTCGTTCAAAGTCAGTGCAATGGCTTCTTACTTCCTTAATTCAAGT
                                                                                                                                                                                                                                            77 HisHisAlaIleLeuThrProLeuGlnThrHisLeuThrMetLysGlySerSerMetLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovine EST associated with lactation/muscle/fat deposition #9738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Warren
(1-133462)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9724 CATCCCTCCCAAGTCATC 9707
US-09-974-546C-84 (1-135) x ABD32622
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                                                                                                                                                                                                                                                                 9838 AATTATGCTGTT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 HisPro---Gluileile 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABX44573 standard; cDNA; 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-JAN-1999; 99US-0115707P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-FEB-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BYAT/) BYATT J C.
(MATH/) MATHIALAGAN N
(TAON/) TAO N.
(WARR/) WARREN W C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VPI; 2003-110599/10.
                                                                                                                                                                                                                                                                                                                                                                                                                      9751 TTAAGG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABX44573;
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from base 900001 (Thermococcus kodakaraensis KOD1 LOCUS ADN47591 Accession Adn47591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68543 ACTAATGATCTAAAAACGGGAAAAGGAAAAAGAGCTTGAAGAGCTGGGGGTAGGATTGGTT 68484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 SerSerMet---LysCysSerSerLeuSerSerGluAlalleLeuPheThrLeuThrLeu 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----AsnPhePro 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 ArgLeuProGlyIleLeuAlaProGluThrValLeuLeuProPheCysTyrLysValPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 ArglyslysGluLysVallysArgSerGlnLysAlaThrGluPhe---IleAspTyrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 IleGluGlnSerHisHisAlaIleLeuThrProLeuGlnThrHisLeuThrMetLysGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 MetHisAsnIleIleHisIleLeuGlnIleArgLysLeuArgHisArgLeuSer----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 GlnLeuThrGlnThrLeuGlyLeuGluCysCysLeuLeu 124
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Mismatches:
Indels:
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Matches:
                                                                                              1210000
1310000
1410000
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1610000
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11 fragments
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81.00
44.36%
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1200001
1300001
1400001
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Continuation (10 of 21) of A
WP Sequence split into 21 fr
WP ADN47591_01
WP ADN47591_01
WP ADN47591_03
WP ADN47591_03
WP ADN47591_04
WP ADN47591_06
WP ADN47591_06
WP ADN47591_06
WP ADN47591_06
WP ADN47591_07
WP ADN47591_07
WP ADN47591_07
WP ADN47591_08
WP ADN47591_09
WP ADN47591_09
WP ADN47591_10
WP ADN47591_11
110
WP ADN47591_11
                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
ADN46845 06
ADN46845 07
ADN46845 08
ADN46845 10
ADN46845 11
ADN46845 13
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ADN46845 14
ADN46845 14
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                                                                 cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nuclectide sequences, appearing as ABX44836-ABX49947, or complements of them. Also included are (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non- translated sequence that call the cell to cause termination of transcription and addition of polyadenylated ribonuclectides to a 3' end of the mRNA molecule; and of polyadenylated ribonuclectides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid is predictive of the complementary nucleic acid is molecule; and detection of the molecule. The LMFD nucleic acid is predictive of the detection of the molecule in a bovine cell or tissue.

It is useful for genome mapping, gene identification and analysis, cattle breathing a level or pattern of a molecule in a bovine cell or tissue. The present sequence was not shown in the present sequence is one of the plant proper forms from the present sequence is one of the plant proper.
                                                     invention relates to a purified nucleic acid molecule associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 AAAGGTTTGCCAACCCGTTCGCCCGTACACCTGCCCCGTTTCACGATGCAACCTGCTTCT 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                 Claim 2; SEQ ID NO 9738; 245pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      format from the USPTO web si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-974-546C-84 (1-135) x ABX44573 (1-381)
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11.67$
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ADN46845 11/C
Continuation (12 of 21) o
WP Sequence split into 21
WP Fragment Name
WP ADN46845 00
WP ADN46845 01
WP ADN46845 03
WP ADN46845 03
WP ADN46845 03
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P ADN46845_01
P ADN46845_03
P ADN46845_03
P ADN46845_09
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20991 GTTGTCCACGCCACGCC---TTCACTCCACTCGCTGAAGGCGGTTAAGGCCGGG 21047
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                                                                                                                                                                                                                                                                                                                                                 93 SerSerMet---LysCysSerSerLeuSerSerGluAlalleLeuPheThrLeuThrLeu 111
                                                                                                                                                                                                                                                                                                             73 IleGluGlnSerHisHisAlaIleLeuThrProLeuGlnThrHisLeuThrMetLysGly 92
                                                                                                                                                                                                   ------AsnPhePro 33
                                                                               110000
31
28
42
32
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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1710000
1810000
1910000
2010000
                                                                               5.52e+03
81.00
44.36%
23.31%
11.67%
1400001
1500001
1600001
1700001
1800001
2000001
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Best Local Similarity:
Query Match:
DS:
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ADN47591 14
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Pred. No.:
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Sequence 17253, A
Sequence 17254, A
Sequence 11803, A
Sequence 12923, A
Sequence 16739, A
Sequence 16514, A
Sequence 1252, A
Sequence 1262, A
Sequence 1104, Ap
Sequence 1259, Ap
Sequence 16104, Ap
Sequence 16104, Ap
Sequence 16104, Ap
Sequence 16104, Ap
                                                                                                                                                                                                                                                      Sequence 446, App
Sequence 202994,
Sequence 17253, A
Sequence 17254, A
                                                                                                                                                         Sequence 12551, A
Sequence 12900, A
Sequence 12412, A
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Sequence 25
Sequence 18
                                                                                                                                              Sequence 17
                                                                 Sequence (
                                                                                                                                                                                                                       Sequence 1
Sequence 1
                     Sequence
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ZIP: 77210

MEDIUM TYPER FORM:
MEDIUM TYPER Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/09/097,199
US-09-949-016-15729

US-09-573-080A-99

US-08-675-566-15

US-08-675-566-13

US-08-675-566-13

US-08-675-566-13

US-08-675-566-13

US-08-675-566-13

US-08-675-566-13

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US-09-949-016-12000
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PRIOR APPLICATION DATA:
APPLICATION UNDRER:
APPLICATION UNDRER: US 08/692,787
FILING DATE: 31-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: NAKachima, Richard A.
REGISTRATION NUMBER: P-42,023
REFERENCE/DOCKET NUMBER: UROC:018
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                   42672
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19008
160759
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462589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-097-199-83
                 Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/105FV0 spool/US09974546/runat_07092005_174503_21006/app_query.fasta_1.654
-Q=/cgn2 1/105FV0 spool/US09974546/runat_07092005_174503_21006/app_query.fasta_1.654
-DB=Issued_Patents_NA -QFPMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LCOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -NATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL.OUTFPRT=pco -NOFM=ext -HEAPSIZES=500 -MINIENEO -MAXIEN=200000000
-USER-USO9974546 @CGN 1 1 77 @runat_07092005_174503_21006 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQÜERY -NĒG SCÖRES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMBOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83, Appl
85, Appl
3311, Ap
115053, A
119365,
119366,
119364,
148, App
                                                                                                           15 ; Search time 104.5 Seconds (without alignments) 2113.850 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/eCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                            OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-097-199-85
US-09-949-016-3311
US-09-949-016-119365
US-09-949-016-119365
US-09-949-016-119364
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US-09-248-796A-148
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US-09-186-188B-53
US-09-265-585C-53
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                                                                                                                                                                                                                                                                                                                                1202784 seqs, 818138359 residues
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                                                                                                           September 9, 2005, 13:12:05
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Database :

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Searched:

Title: Perfect score:

Run on:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: An, Gang
APPLICANT: O'Hara, S. Mark
APPLICANT: O'Hara, S. Mark
APPLICANT: Ralph, David
APPLICANT: Velti, Robert
TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
TITLE OF INVENTION: PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Arnold, White & Durkee P.O. Box 4433
INFORMATION FOR SEQ 10 0 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 2087 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
FRATURE:
NATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 85, Application US/09097199 Patent No. 6218529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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694.00
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100.00%
                                                                                                                               NAME/KEY: CDS
LOCATION: 99..503
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Best Local Similarity:
Query Match:
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STREET: P.O. Bo
CITY: Houston
STATE: Texas
COUNTRY: USA
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Pred. No.:
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US-09-097-199-85
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RESULT 3
US-099-016-3311
US-09-949-016-3311, Application US/09949016
; Sequence 3311, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218
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                     PatentIn Release #1.0, Version #1.30
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                            CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,787
FILING DATE: 31-UUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Nakashima, Richard A.
REGISTRATION NUMBER: P-42,023
REFERENCE/DOCKET NUMBER: UROC:018
TELECHANICATION INFORMATION:
TELECHANICATION INFORMATION:
TELECHANICATION INFORMATION:
TELECHANICATION INFORMATION:
TELECHANICATION INFORMATION:
TELECHANICATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 2505 base pairs
                  SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,199
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       694.00
100.00%
100.00%
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STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , NAME/KEY: CDS
; LOCATION: 99...
US-09-097-199-85
                                                                             FILING DATE
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Best Local Similarity:
Query Match:
DB:
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US-09-949-016-119365
                                                                     ORGANISM: Human
US-09-949-016-15053
                                                                                                                                    Alignment Scores:
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Score:
                                                 TYPE: DNA
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Sequence 15053, Application US/09949016

Sequence 15053, Application US/09949016

Sequence 15053, Application US/09949016

Sequence 15053, Application US/09949016

SERBAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR APPLICATION UNDHERE: 60/231,498

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
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                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PSELSEQ for Windows Version 4.0
SERIGTH: 2506
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Human
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Pred. No.:
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US-09-949-016-119365/c

US-09-949-016-119365/c

Sequence 119365, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOOU307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PLILING DATE: 2000-10-20

PRIOR PLILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 2007012

SOFTWARE: PESECS for Windows Version 4.0

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Matches:
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 15053
LENGTH: 6507
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61 ArgSerGlnLysAlaThrGluPheIleAspTyrSerIleGluGlnSerHisHisAlaIle
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Best Local Similarity:
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; ORGANISM: Human
US-09-949-016-119364
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Pred. No.:
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| Sequence 119366, Application US/09949016
| Patient No. 681239
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al. |
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES 2000-04-14 |
| FRICH APPLICATION NUMBER: 60/241,755 |
| PRIOR PELLING DATE: 2000-10-03 |
| PRIOR PELLING DATE: 2000-10-03 |
| PRIOR PELLING DATE: 2000-10-03 |
| PRIOR PELLING DATE: 2000-10-03 |
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| PRIOR PELLING DATE: 2000-10-03 |
| PRIOR PELLING DATE: 2000-10-03 |
| PRIOR PELLOATION NUMBER: 60/231,498 |
| NUMBER OF SEQ ID NOS: 207012 |
| SEQ ID NO 113366 |
| LENGTH: 601 |
| LENGTH: 601 |
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Best Local Similarity:
Query Match:
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US-09-949-016-119366/c
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US-09-949-016-119366
Percent Similarity:
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US-09-949-016-119364/C

| Sequence 1193564/C
| Sequence 1193564/C
| Sequence 1193564, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| CURRENT PAPLICATION NUMBER: US/09/949,016
| CURRENT PILING DATE: 2000-04-14
| PRIOR FILING DATE: 2000-10-03
| PRIOR PILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SOFTWARE: FastSEQ for Windows Version 4.0
| LENGTH: 601
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21 GlnIleArgLysLeuArgHisArgLeuSerAsnPheProArgLeuProGlyIleLeuAla
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597 CACTAIG------TCTCTIGCTACACAGIGITGTTCTGCGCTGAITCT 556
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                          and Uses
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APPLICANT: Helariutta, Yrjo
TITLE OF INVENTION: Scarcerow Gene, Promoter and
FILE REFERENCE: 5914-075-999
CURRENT APPLICATION NUMBER: US/09/186,276B
CURRENT FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: 08/642,445
PRIOR FILING DATE: 1997-04-24
PRIOR APPLICATION NUMBER: 08/638,617
PRIOR FILING DATE: 1996-04-26
NUMBER OF SEQ ID NOS: 79
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 53
LENGTH: 1093
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Indels:
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TITLE OF INVENTION: Scarecrow Gene, Promoter;
TITLE OP INVENTION: Thereof
FILE REFERENCE: 5914-056-999
CURRENT APPLICATION NUMBER: US/08/842,445A
CURRENT FILING DATE: 1997-04-24
EARLIER APPLICATION NUMBER: 08/638,617
EARLIER FILING DATE: 1966-04-26
NUMBER OF SEQ ID NOS: 79
                                                                                                                                                                                                                                                                                                                                                                                                              Matches:
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                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 uTyrLeuSer 127
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Query Match:
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US-08-842-445-53/c
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                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR PILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO: 28208
LENGTH: 2472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1871 TCCAAGTTATTCCAACTTTTGGTCATTTGATCACCTTCAATTCTGGTAAATCTCAAAACT 1930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1931 CCTTTGCTAAATTGTTACGTAACTTCAACCCAATGTTGTTATTACATGGTGAACATTACT 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----SerGluAlaIleLeuPheThrLeuThrLeu 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97
24 LysLeuArgHisArgLeuSerAsnPheProArgLeuProGlyIleLeuAlaProGluThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 ValLeuLeuProPheCys-----TyrLysValPheArgLysLysGluLysVal
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                                                                81 LeuThrProLeuGlnThrHisLeuThrMetLysGly 92
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                        37 CTCACACCTTGCAGACACACTTGACCATGAAAGGT
                                                                                                                                                                                     Sequence 140, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
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Sequence 53, Application US/09186276B
Patent No. 6388173
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APPLICANT: Benfey, Philip
APPLICANT: Dilaurenzio, Laura
APPLICANT: Wysocka-Diller, Joanna
APPLICANT: Malamy, Jocelyn E.
APPLICANT: Pysh, Leonard
                                                                                                                                                                                                                                                          APPLICANT: Keith Weinstock et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.697
83.50
44.17%
29.17%
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Best Local Similarity:
Query Match:
                                                                                                                                                                      US-09-248-796A-148
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Pred. No.:
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753 GITTIGICATAAGCTITCAGCAICTCACTCGCTGCAAACGCTGCAGATGTGCTGACCGG 694
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-----CATTCTGACCCT 658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       921 TACAGCGACAGATGTGTTTTTTTGTTGTCTCTTTTTTCCACTCAAGTAACCATCATCAC 862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 TyrLysValPheArgLysLysLysGluLysValLysArgSerGlnLysAlaThrGluPhelle 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 861 TATAACTTACCCAATATAGTTTGGGTTTCGCTTCCACACGGAACA------TGT
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1 Sequence 53, Application US/09186188B

1 Patent No. 6455672

2 GENERAL INFORMATION:

2 GENERAL INFORMATION:

3 APPLICANT: Beney et al.

3 TITLE OF INVENTION: Thereof

3 TITLE OF INVENTION: Thereof

3 TITLE OF INVENTION: Thereof

4 TITLE OF INVENTION: Thereof

5 TITLE REFERENCE: 5914-074-99

5 CURRENT APPLICATION NUMBER: US/09/186,188B

7 CURRENT PILING DATE: 1998-11-05

7 PRIOR APPLICATION NUMBER: 08/642,445

7 PRIOR APPLICATION NUMBER: 08/638,617

7 PRIOR APPLICATION NUMBER: 08/638,617

7 PRIOR APPLICATION NUMBER: 08/638,617

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7 PRIOR APPLICATION NUMBER: 08/638,617
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37
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Matches:
Conservative:
Mismatches:
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) SOFTWARE: FastSEQ for Windows Version 3.0 ; SEQ ID NO 53 
LENGTH: 1093 
; TYPE: DNA ; ORGANISM: Plant 
US-08-842-445-53
                                                                                                                                                                                                                                                                                                                                Gaps:
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80.50
36.81%
25.69%
11.60%
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555 CTGCTTATCA 546
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597 CACTATG-----
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	BArgLeu TCATCAC	roPheCys TGT	luPheile :: ::: AGTTTGTA		His-LeuThrMe :: CATTCTGACCCT	lereuPh ::: \TCATGTT	Leule ::: CTGATTCT			
	-84 (1-135) x US-09-186-188B-53 (1-1093) TyrGluAspMetHisAsnIlelleHisIleLeuGlnIleArgLysLeuArgHisArgLeu TyrGluAspMetHisAsnIleIleHisIleLeuGlnIleArgLysLeuArgHisArgLeu TyrGAGGACAAGATGTGTTTTTGTTGTGTTCTTTTTTTTTTT	aProGluThrValLeuLeuProPh 	TyrLysValPheArgLysLysGluLysValLysArgSerGlnLysAlaThrGluPheIle :::	ABDTyrSerile	nThrHis-L CATTC	LysGlySerSerMetLysGysSerSerLeuSerSerGluAlalleLeuPh 	hrleuglyLeuglucyscysLeule :: ::: ::: crcrrgcracagrerrgrrcrgcgcrgarrcr		Thereof	
1093 37 16 44 6	eArgLy	luThrVa.	sVallysArgSerGlnLysAl : ::: GGTAGAGGCTCCTTCATGGC	ACGCTG	eLeuThrProLeuGlnThrHi CA	SerSe	lucysc: ::[:AGTGTT		Uses	1093 37
s: vative ches:	(1-109)	laProg] TTCCAC	ysArgSe :: !AGCGCTC	GCTGCA	euThrP	CTCTCTC	euGlyLeuGluCy TTGCTACACAGTG		er and	:: 81
Length: Matches: Conservati Mismatches Indels:	-188B-53 eHisileL : ::: rGrGCTCT	::: GTTTGGG	Lysvall ::: : GAGGTAG	CTCACTC	Alail	rSerteu CTCTACT	nThrieu ::: -TCTCT		Promoter 65,585C	Length: Matches:
	-09-186- snilelle :::	auProGly :: :AGTTTGC	/BLYBGlu TCCAGAA	TCAGCAT	rHisHisAl	yscyssers ccrcrcrcr	euThrG		,/09265585, N. N. Laura m E. Tjo rrow Gene, 1: 08/09/2 08/842,44 1: 24 08/638,61 09 06/638,61	
0.5 80.50 36.81% 25.69% 111.60%	4 (1-135) x US-09- rGluaspMetHisAsnIl CAGCGACAGATGTGTTTT	SerAsnPheProArgLeuProGlyIleLeuAlaProGluThrVal 	TyrLysValPheArgLysLysGluLy :: AGCCATGGGTCGTCTTCCAGAAGA	[]e	GluGlnSerHisHis CCAACCCGTGAACCCAGCCATCAT	rSerMetLysCy AGTACCTCGTG	eThrLeuThrLeuGlnLeuThrGlnThrL ::: CACTATGTCTC	r 127 546		0.5 80.50
ty: arity:	4 (1-135) rGluAspMe	rAsnPhe TAACTTA	rLysVal	AspTyrSeril ::: GTTTTTGTCAT		ysGlySerS ATTTCCCA	eThrLeuTh ::: CACTATG	uTyrLeuSer 	25-585C-53/c to 680234 L INFORMATION: (CANT. Benfey, Phillip); (CANT. Benfey, Phillip); (CANT. Benfey, Poillip; (CANT. Malamy, Jocelyn; (CANT. Malamy, Jocelyn; (CANT. Pysh, Leonard, (CANT. Bruce, Wesley, (CANT. Bruce, Wesley, (CANT. Lim, Jun CANT. Ling DATE: 1996-04-38 CA PELICATION NUMBER: 0 CA FILING DATE: 1996-04-38 CA PELICATION NUMBER: 0 CA PELICATION NUMBER: 0 CA PELICATION NUMBER: 0 CANT. AND CANT. CA	
: imilari 1 Simil. ch:	-974-546C-84 10 TYr 921 TAC	30 Se 861 TA	50 TY 813 AG	70 AS	74 693 CC	90 tLy	107 eT	124 uT 555 CT	-585C-53/C -6.53/Applice -6.6.8. Applice -6.6.9. Applice -6.6.9. Applice -6.6. Applice -6.6. Applice -6.6. Applice -6.6. Application -6.6. Application -6.6. Application -6.6. Application -6.	Scores:
No.	60-								SULT 1 09-26 Sacquer Sacquer Sacquer Sacquer Sacquer Sacquer APPLI	Alignment Pred. No.: Score:
Pred Score Perce Best Query DB:	Sn o	\$ A	ço da	<i>장</i> 음	S G	දි දි	\$ B	\$ <u>8</u>	8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Pre

Percent Similarity: 36.81% Conservative: 16 Best Local Similarity: 25.69% Mismatches: 47 Query Match: 11.60% Indels: 44 Gaps: 6	Ouery Match: 11.53% Indels: 29 DB: 4 Gaps: 4 US-09-974-546C-84 (1-135) x US-09-949-016-15729 (1-148783)
US-09-974-546C-84 (1-135) x US-09-265-585C-53 (1-1093)	Oy 5 LeuargasnGlnLysTyrGluaspWetHisasnileileHisileLeuGlnIleArgLys 24
Oy 10 TyrGluaspMetHisAsnIleIleHisIleLeuGlnIleArgLysLeuArgHisArgLeu 29	Db 15651 CTTCATGACAATCCATATAAAGATACCACTATTATTATCCACATTTTACAGATAAGAAAA 15592
921 TACAGCGACAGATGTTTTTTTTTTTTTTTTTTTTTTTTT	25 LeuArgHisArgLeuSerAsnPheProArgLeuProGlyIleLeuAlaProGluThrVal
GY 30 SerABRPHSPROADSTALEMENTAGE AND APPOGLATHRYBILEULEULPOPHOCYS 49 DD 861 TATAACTTACCCAATATAGTTTGGGTTTGGCTTCCACACGGAACATGT 814	Db 15591 CTGAGGCACAGAGA-CTAAATAAATCTAAATTCCCACAGGTAGTAAGT 15545 Qy 45 LeuLeuProPheCysTyrLysValPheArgLysLysGluLysValLysArgSerGlnLys 64
Qy 50 TyrLysValPheArgLysLysGluLysArgSerGlnLysAlaThrGluPhelle 69	Db 15544
Db 813 AGCCATGGGTCGTCTTCCAGAAGAGGTAGAGCGCTCCTTCATGGCCTCCCAGTTTGTA 754 Qy 70 ABpTyrSerile73	Qy 65 AlaThrGluPheIleAspTyrSerIleGluGlnSerHisAlaIleLeuThrProLeu 84
Db 753 GTTTTGTCATAAGCTTTCAGCATCTCACTGCAAACGCTGCAGATGTGCTGACCGG 694	Qy 85 GlnThrHisLeuThrMetLysGlySerSerMetLysCysSerSerLeuSer 101
74GluGlnSerHisHisAlalleLeuThrProLeuGlnTh	Db 15467 TCAACGCATTCCCAAATGGAGCAGGAGAATAAGCGCCAGCAACAACAAAGGAGACAT 15408
693 CCAACCCGTGAACCCAGCCATCATCATTCTGACCCT	102SerGluAlaIleLeuPheThrLeuGhrLeuGlnLeuThrGlnThrLeu
OY UNSELYSETSETMETLYBCYBSETSETLEUSETSETGLUALALLEURIN 107	DB 15407 CGACGCCAAAGGTCTACCATAAAGTTTTTCACGGTCATCCTTGCTTACCTGT 15354 OV 118 GlyLeuGluCySCYSLeuLeuTyrLeuSerLysThrIleHisPro 132
	15353 CCAGGCCATGCTTGGCATACTCCTCCCAAACCCGGGGACCC
Db 597 CACTAIGTCTCTTGCTACACAGTGTTGTTCTGCGCTGAITCT 556	RESULT 14
24 uTyrLeuSer	US-09-5/3-080A-99/C ; Sequence 99, Application US/09573080A ; Patent No. 68280997.
DD 555 CIGCITAICA 546	; GENERAL INFORMATION: ; APPLICANT: JOAN, KNOLL
REGULT 13 US-09-949-016-15729/C ; Pacence 15729, Application US/09949016 ; Patent No. 6812339 ; GENERAL INFORMATION:	; APPLICANT: ROGAN, PETER ; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATIN ; FILE REFERENCE: 30307 ; CURRENT APPLICATION NUMBER: US/09/573,080A ; CURRENT FILING DATE: 2000-05-16
	; NUMBER OF SEQ ID NOS: 479 ; SOFTWARE: PatentIn version 3.0 ; SEQ ID NO 99
; FILE REFERENCE: CL001307 ; CURRENT APPLICATION NUMBER: US/09/949,016	; LENGTH: 262 ; TYPE: DNA
; COKKENI FILING DATE: 2000-04-14; PRIOR APPLICATION UNBER: 60/241,755	CACANISM: Homo sapiens FEATURE:
	; NAMES AND TERROR ENDING ; LOCATION (1): (52) ; OTHER INFORMATION: mir
APPLICATION NUM FILING DATE: 20	:
; NUMBER OF SEQ ID NOS: 207012 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 15729	; AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A ; TITLE: Prototypic sequences for human repetitive DNA ; JOURNAL: Journal of Molecular Evolution
LENGTH: 14 TYPE: DNA	••
<pre>// OKABULAN: Human // FEATURE: // NAME/KEY: misc feature // LOCATION: (1)(148783) // OTHER INFORMATION: n = A,T,C or G US-09-949-016-15729</pre>	PAGES: 286-291 ; DATE: 1992-10- ; DATABASE ACCESSION NUMBER: Database of repetitive elements (repbase) ; DATABASE ENTRY DATE: 1996-01-26 ; DATABASE ENTRY DATE: 1996-01-26
Alignment Scores: Pred. No.: Pred. No.: Score: Score: Percent Similarity: Best Local Similarity: 30.37% Mismatches: 52	Alignment Scores: 0.0721 Length: 262 Pred. No.: 79.50 Matches: 27 Percent Similarity: 46.67% Conservative: 1 Best Local Similarity: 45.00% Mismatches: 10

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fischer, Laurent
TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,
TITLE OF INVENTION: RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF
TITLE OF INVENTION: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1747 TACAAAGACCTGCATCCCTTCGTTAGC-----AGACAGCTCTTGCACACGC 1794
                                                                                                                     174 CAACCCTATGAGGTAGGTACTATTATTCCCCATTTTACAGATGAGGAAACTGAGGCAC 115
                                                                                   GinLysTyrGluAspMetHisAsnIleIleHisIleLeuGlnIleArgLysLeuArgHis 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 TyrGluAspMetHisAsnIleIleHisIleLeuGlnIleArgLysLeuArgHisArgLeu 29
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                                                                                                                                                           -----3er 30
                                                                                                                                                                                          114 AGAGAGGTTAAGTAACTTGCCCAAGGTCACACAGGCTAGTAAGTGGCAGAGCCGGGATTCG 55
                                                                                                                                                                                                                            31 AsnPheProArgLeuProGlyIleLeuAlaProGluThrValLeuLeu-ProPheCys 49
                                                                                                                                                                                                                                                  54 AAC------CCAGGCAGTCTGGCTCCCAGAGYCCGTGCTCTTAACCACTATGC 9
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30
28
48
19
 222
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MEDIUM TYPE: Floppy disk
COMPUTER: TBM FC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,566
FILING DATE: 03-UUL-1996
CLASSIFICATION: 424-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                US-09-974-546C-84 (1-135) x US-09-573-080A-99 (1-262)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: United States of America
 Indels:
Gaps:
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REPERENCE/DOCKET NUMBER: 454310
TELECOMMUNICATION INFORMATION:
                                                                                                                                                         28 ArgLeu-----
                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08675566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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SEQUENCE CHARACTERISTICS:
LENGTH: 6196 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (212)840-3333
(212)840-0712
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46.40%
24.00%
11.46%
11.46%
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Best Local Similarity:
Query Match:
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Pred. No.:
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Query Match:
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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2005, 14:46:00 ; Search time 408.5 Seconds (without alignments) 2170.324 Million cell updates/sec
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OM protein - nucleic search, using frame_plus_p2n model
                                                                                                               US-09-974-546C-84
                                       ď
                                       September
                                                                                                             Title:
Perfect score:
                                                                                                                                                    Sequence:
                                     Run on:
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0.5 0.5 0.5 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

BLOSUM62

Scoring table:

Total number of hits satisfying chosen parameters:

7351250 segs, 3283620254 residues

Searched

14702500

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Database :

Published Applications NA:*

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/pubpna/US11A PUBCOMB.seq:/
/pubpna/US11 NEW PUB.seq:*/
/pubpna/US60 NEW PUB.seq:* ptodata/2/ ptodata/2, ptodata/2, /cgn2_6/1 /cgn2_6/1 /cgn2_6/1 /cgn2_t

is the number of results predicted by chance to have a Pred. No.

/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seg:*

ptodata/2/pubpna/US60

ptodata/2/pubpna/US11

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1 694 100.0 2007 10 US-09-74-546-83 Sequence 2 694 100.0 2007 10 US-09-74-546-85 Sequence 3 12.0 1133 1 US-01-159-493-4085 Sequence 3 12.0 1136 17 US-01-369-493-2501 Sequence 3 12.0 14644 15 US-01-017-128-1 8 12.0 14644 15 US-01-017-128-1 8 12.0 14644 15 US-01-017-128-1 8 12.0 14644 15 US-01-017-128-1 8 20 13.0 11.1 8 11.7 133462 19 US-09-00-92-3138 Sequence 8 11.7 133462 19 US-09-00-92-3138 Sequence 11.8 11.7 133462 19 US-09-00-92-3138 Sequence 12.8 11.7 133462 19 US-09-00-92-3138 Sequence 13.8 11.7 133462 19 US-09-00-92-3138 Sequence 14.8 00.5 11.6 60.0 22 US-10-425-115-137953 Sequence 15.8 00.5 11.6 60.0 22 US-10-425-115-137953 Sequence 16.0 0.5 11.6 60.0 22 US-10-425-115-137953 Sequence 17.0 0.5 11.6 1026 18 US-10-425-115-137953 Sequence 18.0 0.5 11.6 60.0 22 US-10-425-115-137953 Sequence 18.0 0.5 11.6 60.0 22 US-10-25-10-13799 Sequence 18.0 0.5 11.6 60.0 22 US-10-25-10-31309 Sequence 18.0 0.5 11.6 60.0 22 US-10-25-10-31309 Sequence 18.0 0.5 11.6 1026 18 US-10-425-115-13794 Sequence 18.0 0.5 11.6 1029 9 US-09-16-25-10-31309 Sequence 18.0 0.5 11.6 60.0 20 US-10-425-10-31309 Sequence 18.0 0.5 11.6 60.0 20 US-10-425-10-31309 Sequence 18.0 0.5 11.6 1039 9 US-09-16-26-26-31309 Sequence 18.0 0.5 11.5 September 18.0 0.5	1 694 100.0 2007 10 US-09-74-546-83 Sequence 2 694 100.0 2007 10 US-09-74-546-83 Sequence 3 120 1113 17 US-10-169-493-4085 Sequence 8 12 12 15 1624 20 US-10-459-491 8 12 12 1644 10 US-09-77A-223 Sequence 8 12 12 1644 10 US-09-70-45-115 49918 Sequence 9 11.7 133462 19 US-10-455-115-49918 Sequence 12 11.7 133462 19 US-09-70-97A-23 Sequence 13 12 11.7 133462 19 US-09-70-97A-23 Sequence 14 11.7 133462 19 US-09-70-97A-23 Sequence 15 11.7 133462 19 US-09-70-97A-23 Sequence 16 11.7 133462 19 US-09-70-978-93 Sequence 17 11.7 133462 19 US-09-70-978-93 Sequence 18 11.7 17 437 20 US-10-425-115-137993 Sequence 18 11.7 437 20 US-10-425-115-137993 Sequence 18 11.7 437 20 US-10-425-115-137993 Sequence 18 11.7 437 20 US-10-425-115-137993 Sequence 18 11.7 437 20 US-10-425-115-137993 Sequence 18 11.7 437 20 US-10-425-115-137993 Sequence 18 11.7 437 20 US-10-425-115-137993 Sequence 18 11.7 437 20 US-10-425-115-137993 Sequence 18 11.8 11.1 4 10.0 10.0 10.0 10.0 10.0 10.0 10	Result No.	Scor	Ouery Match	Length	DB		cription
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39 78.5 11.3 1787 13 US-10-027-632-84670 Sequence 84670, 40 78.5 11.3 1787 17 US-10-027-632-84669 Sequence 84669, 41 78.5 11.3 1787 17 US-10-027-632-84670 Sequence 84669, 42 78 11.2 650 13 US-10-027-632-233621 Sequence 223621, 43 78 11.2 650 17 US-10-027-632-233621 Sequence 223621, 44 78 11.2 9869 20 US-10-424-599-5755 Sequence 23555, A4 78 11.2 1207 18 US-10-424-599-5755 Sequence 23555, A5 78 11.2 1207 18 US-10-424-599-5755 Sequence 235321, 45 78 11.2 1207 18 US-10-424-599-5755 Sequence 235321, 45 78 11.2 1207 18 US-10-424-599-5755 Sequence 235321, 45 78 11.2 1207 18 US-10-424-599-5755 Sequence 235321, 45 78 11.2 1207 18 US-10-424-599-5755 Sequence 235320, 45 78 11.2 1207 18 US-10-424-599-5755 Sequence 235320, 45 78 11.2 1207 18 US-10-424-599-5755 Sequence 235320, 45 78 11.2 1207 18 US-10-424-599-5755 Sequence 2555, A5 78 11.2 1207 18 US-10-424-599-5755 Sequence 2555, A5 78 11.2 1207 18 US-10-424-599-5755 Sequence 2555, A5 78 11.2 1207 18 US-10-424-599-5755 Sequence 2555, A5 78 11.2 1207 18 US-10-424-599-5755 Sequence 2555, A5 78 11.2 1207 18 US-10-424-599-5755 Sequence 2555, A5 78 11.2 1207 18 US-10-424-599-5755 Sequence 2555, A5 78 11.2 1207 18 US-10-424-599-5755 Sequence 2555, A5 78 11.2 1207 18 US-10-424-590-5755 Sequence 2555, A5 78 11.2 1207 18 US-10-425-115-115430 Sequence 2555, A5 78 11.2 1207 18 US-10-425-115-115430 Sequence 2555, A5 78 11.2 1207 18 US-10-425-115-115430 Sequence 2555, A5 78 11.2 1207 18 US-10-425-115-115430 Sequence 2555, A5 78 11.2 1207 18 US-10-425-115-115410 Sequence 2555, A5 78 11.2 1207 18 US-10-425-115-115410 S	39 78.5 11.3 1787 13 US-10-027-632-84670 Sequence 84670, 40 78.5 11.3 1787 17 US-10-027-632-84669 Sequence 84669, 41 78.5 11.3 1787 17 US-10-027-632-84669 Sequence 84669, 42 78 11.2 650 13 US-10-027-632-23621 Sequence 223621, 43 78 11.2 650 17 US-10-027-632-23621 Sequence 223621, 44 78 11.2 1207 18 US-10-424-599-5755 Sequence 5755, A 11.2 9869 20 US-10-425-115-139430 Sequence 139430, A 11.2 9869 20 US-10-425-115-139430		78		1787	13	-10-027-632-8466	equence 84669,
40 78.5 11.3 1787 17 US-10-027-632-84669 Sequence 84669, 41 78.5 11.3 1787 17 US-10-027-632-84670 Sequence 84670, 42 78 11.2 650 13 US-10-027-632-223621 Sequence 223621, 43 78 11.2 650 17 US-10-027-632-223621 Sequence 223621, 44 78 11.2 1207 18 US-10-424-599-5755 Sequence 139430, 45 78 11.2 9869 20 US-10-425-115-139430 Sequence 139430,	40 78.5 11.3 1787 17 US-10-027-632-84669 Sequence 84669, 41 78.5 11.3 1787 17 US-10-027-632-84670 Sequence 84670, 42 78 11.2 650 13 US-10-027-632-23621 Sequence 223621, 43 78 11.2 650 17 US-10-027-632-223621 Sequence 223621, 44 78 11.2 1207 18 US-10-424-599-5755 Sequence 23551, A5 78 11.2 9869 20 US-10-425-115-139430 Sequence 139430, ATTOMORMS		78		1787	13	.0-027-632-8467	equence 84670,
41 78.5 11.3 1787 17 US-10-027-632-84670 Sequence 84670, 42 78 11.2 650 13 US-10-027-632-223621 Sequence 223621, 43 78 11.2 650 17 US-10-027-632-2233621 Sequence 223621, 44 78 11.2 1207 18 US-10-424-599-5755 Sequence 139430, 45 78 11.2 9869 20 US-10-425-115-139430 Sequence 139430,	41 78.5 11.3 1787 17 US-10-027-632-84670 Sequence 84670, 42 78 11.2 650 13 US-10-027-632-223621 Sequence 222621, 43 78 11.2 650 17 US-10-027-632-223621 Sequence 223621, 44 78 11.2 1207 18 US-10-424-599-5755 Sequence 5755, A 11.2 9869 20 US-10-425-115-139430 Sequence 139430, A 11.2 9869 20 US-10-425-115-139430		78		1787	17	0-027-632-8466	equence 84669,
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	SHADAWAY T TA			•	96	20	-10-425-115-13943	equence 139430,
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O'Hara, S. Mark
Ralph, David
Veltri, Robert
TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE Sequence 83, Application US/09974546 Publication No. US20030050470A1 GENERAL INFORMATION: APPLICANT: An, Gang US-09-974-546-83

CORRESPONDENCE ADDRESS: ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston NUMBER OF SEQUENCES: 87

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158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          399 TCTTCAGAAGCCATATTATTCACATTGACTTTGACTTAGCTCAGACCCTAGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 ATGAGGGCCTTCTTAAGGAACCAGAATATGAGGATATGCACAATATTCACATTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ArgSerGlnLysAlaThrGluPhelleAspTyrSerIleGluGlnSerHisHisAlaIle
                                                                COMPUTER: ISM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/974,546
FILING DATE: 10-Oct-2001
CLASSIFICATION: Unknown
PRIOR APPLICATION UNKNOWN
APPLICATION NUMBER: 09/097,199
FILING DATE: 1998-06-12
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CysCysLeuLeuTyrLeuSerLysThrileHisProGlnileile 135
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                    NAME: Nakashima, Richard A.
REGISTRATION NUMBER: P-42,023
REGISTRATION NUMBER: P-42,023
REGISTRATION NUMBER: P-42,023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPAX: (512) 414-7577
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 2087 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 99..503
SRQUENCE DESCRIPTION: SEQ ID NO: 83:
                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.82e-85
694.00
100.00%
100.00%
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE
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RESULT 2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ArgSerGlnLygAlaThrGluPhelleAspTyrSerIleGluGlnSerHisHisAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 GlnIleArgLysLeuArgHisArgLeuSerAsnPheProArgLeuProGlyIleLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 CAGATCAGAAATTGAGGCACAGATTAAGTAACTTCCCAAGGCTACCAGGCATTCTAGCT
              Sequence 85, Application US/09974546
Publication No. US20030050470A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: An, Gang
O'Hara, S. Mark
Ralph, David
Veltri, Robert
TITLE OF INVENTION: BLOWARKERS AND TARGETS FOR DIAGNOSIS,
PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
NUMBER OF SEQUENCES: 87
CORRESPONDENCE: ADDRESS:
ADDRESSEE: ALTOId, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: ISEN COMPUTER: ALCOMENTER: TALONGY WISE COMPUTER: IBM PC COMPUTER: DESCRIBED BY COMPUTER: IBM PC COMPUTER: DSCRIBED BY COMPUTER: DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/974,546

FILING DATE: 10-0ct-2001

CLASSIFICATION TOKENOM

APPLICATION DATA:

APPLICATION NUMBER: 09/097,199

FILING DATE: 1998-06-12

ATTORNEY/AGENT INFORMATION:

NAME: NAKABATION:

RECIFICATION NUMBER: P-42,023

RECIFICATION NUMBER: P-42,023
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 2505 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.74e-85
694.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                      STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
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Best Local Similarity:
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US-09-974-546-85
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Command line parameters:
-MODEL=frame.pd. model.-DEV=xlh
-MODEL=frame.pd. model.-DEV=xlh
-MODEL=frame.pd. model.-DEV=xlh
-MODEL=frame.pd. model.-DEV=xlh
-DB=EST -QFWT=fastap -SUFFTX=P2D.rst -MINWATCH=0.1 -LOOFCL=0 -LOOFEXT=0
-UNITS=bite -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bite -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE_pct -THR_MAX=100 -TR_MIN_EN=0 -ALIGN=15 -MODE=LOCAL
-USTR=-DCO-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USTR=-USOP974546 @CGN 1 1 3556 @runat 07092005 174502 20989 -NCPU=6 -ICPU=3
-NO WAAP -LARGEQUER -NEG SCORESC - WAIT -DSPETCKE=100 -LONGLOG
-DEV TIMEOUT=120 -WAAN TIMEOUT=30 -TRIREADS=1 -XGAPOP=10 -KGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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BW557636 BW557636
BW582739 BW582739
BW591794 BW591794
BU413225 603155489
BU436282 603209819
CV511381 kc46008.9
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BW569427 BW569427
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                                                                                                                                                                                                                                                                                                                        1 MRAFLRNQKYEDMHNIHIL......TLGLECCLLYLSKTIHPQII 135
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Compugen Ltd
                                                                                                                                                                                    - nucleic search, using frame_plus_p2n model
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                                                                                                                GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                       9, 2005, 13:09:35
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Maximum Match 100%
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
on Sep 12 09:59:38 2005
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seq length: 200000000
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9b_htc:;
9b_htc:;
9b_est43:;
9b_est6;;
9b_9ss1:;
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8 BH55 9 AG37 5 BX75 9 CR26 3 AY43 5 BO59	, , , , , , , , , , , , , , , , , , , ,	0 4 C C I C A 4 C C C C	COORDINGS COORDI
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ALIGNMENTS

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BUZ42169 690 bp mRNA linear EST 26-NOV-2002
603779592F1 CSEQCHN34 Gallus gallus cDNA clone ChEST725h23 5', mRNA
sequence.
                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 690)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PO Box 88, Manchester, M60 1QD, Tel: 01612008930 Fax: 01612360409
                                                                                                                           GI:25488447
                                                                                                                                                                   Gallus gallus (chicken)
Gallus gallus
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Contact: Simon Hubbard
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                                                                                                          BU242169
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BU242169/c
LOCUS
                                                              DEFINITION
                                                                                                                                                                                     ORGANISM
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JOURNAL
MEDLINE
PUBMED
COMMENT
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AUTHORS
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KEYWORDS
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603155489 603209819 kc40h08.y

CMD29_B11 BW557636

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Alignment Scores:
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AUTHORS
TITLE
JOURNAL
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                                       /dev stage="dult"
/lab_host="bH10B"
/lab_host="bH10B"
/clone lib="CSSECHN14"
/clone lib="CSSECHN14"
/note="Organ: liver; Vector: pBluescript II KS(+); Site_1:
ECORI, Site_2: Not!; This normalized library was
constructed_from 1 million independent clones. CDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
ECORI, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BW569427 Vutaka Satou unpublished cDNA linear EST 31-AUG-2004 BW569427 Yutaka Satou unpublished cDNA library (cstb) Ciona savignyi cDNA clone cstb014a08 3', mRNA sequence.
BW569427.1 GI:51749861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ciona savignyi
Ciona savignyi
Eukaryota: Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 588)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 458 TCAGTTATAAAAGGCCATTTCTCATTTCAGAGCTTTGCTAGGATGCCTCTTCTTATAAGA 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 AsnilelleHisileLeuGlnIleArgLysLeuArgHisArgLeuSerAsnPheProArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||::: ||||||||::: |-----GAT
AACTTAAAATAGCATTTTACGTTTCCCTACAGTTACTAAAGAAATATCAAAT.----GAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398 AAAAAAGGAAAAAGAACACCACCACAAAACTGAGATGCTGCTATTTCTCACTAAATGC
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Matches:
Conservative:
Mismatches:
Indels:
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              /clone="ChEST725h23"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                              1.02
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45.08%
27.05%
13.98%
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REFERENCE

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CB286029 606 bp mRNA linear EST 27-FEB-2003
CMD22 B11_90 UMNMPM3 Sus scrofa cDNA clone PPSUBLIB_15B11 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 AGCAATTTGCACCACGCTATATTTGCAGGGATTCAGTCATTTCTTCCACTGAGTGGCTCA 321
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| CTAGAAGAATCCATITITITIAAAGGACGAAAGCAAAATITACATAATITIGCAATAATCCG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 ThrGlnThrLeuGlyLeuGluCys----- 124
                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="tailbud stage"
/clone_lib="Yutaka Satou unpublished cDNA library (cstb)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55
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Sus scrofa
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
I (bases 1 to 606)
Dvorak, C.M.T., Hyland, K.A., Zhang, Y., Fahrenkrug, S.C. and
Murtaugh, M.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 LysLeuArgHisArgLeuSerAsn------PheProArgLeuProGlyIleLeu 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 AlaProGluThrValLeuLeuProPheCysTyrLysValPhe------ArgLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 LysGluLysValLysArgSerGlnLysAlaThrGluPheIleAspTyrSerIleGluGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 Ser-----HisHisAlaIleLeuThrProLeuGlnThrHisLeuThrMetLysGlySer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     588
37
21
21
25
6
                                                                                                                                                                                                      Email: yutaka@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
Indels:
                                                                                      Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4095
Fax: 81-75-705-1113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 TACTGCTACCTTGTGGATGCTTTTCCTCCACAA 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
                                                                                                                                                                                                                                                      1. .588
/organism="Ciona savignyi"
                       savignyi
                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:51511"
/clone="cstb014a08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-974-546C-84 (1-135) x BW569427 (1-588)
Satou, Y. and Satoh, N. Expressed genes in Ciona Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CB286029.1 GI:28576983
                                                                       Contact: Yutaka Satou
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95.50
44.27%
28.24%
13.76%
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AUTHORS
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0.1.0	ht (c) 1993 - 2005 Compugen Ltd.		
פיזיכסות אמימיסוו מיזים	- 2005		
לעזוניכוע	(c) 1993		
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September 9, 2005, 12:23:48 ; Search time 58 Seconds
(without alignments)
900.218 Million cell updates/sec Run on:

US-09-974-546C-84 Title: Perfect score:

Sequence:

694 1 MRAFLRNQKYEDMHNIHIL.....TLGLECCLLYLSKTIHPQII 135 **BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

2105692 Total number of hits satisfying chosen parameters:

2105692 segs, 386760381 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

A_Geneseq_16Dec04:* Database :

geneseqp1980s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp201s:*
geneseqp202s:*
geneseqp201s:*
geneseqp201s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Aag81358 Human AFP	Adh09599 Human hos	Adh09598 Human hos	Adh09600 Human hos	Aam41462 Human pol	Aab92584 Human pro	Ad197802 Human dcr	Human	Aao15987 Human hel	Abo07204 Human p53		Adn60159 Human hel	Abo64633 Klebsiell	_	Adj69892 Human hea	Ads29846 Bacterial	Aaw30601 Human typ	Adq89904 Antagonis	Aab18292 Plasmodiu	Abb80604 Human sbg
AAG81358	1 ADH09599	1 ADH09598	1 ADH09600	AAM41462	AAB92584	3 ADL97802	AAE09768	. AAO15987	3 ABO07204	ABU64479	ADN60159	/ ABO64633	3 ADM94300	ADJ69892	3 ADS29846	: AAW30601	1 ADQ89904	AAB18292	. ABB80604
424 4	424 8	424 8	424 8	429 4	519 4	1922 8	1924 4	1924 5	1924 6	1924 7	1924 7	438 7	634 8	206 7	982 8	1294 2	1353 8	1398 3	3105 5
10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.1	10.1	10.0	10.0	10.0	10.0
71	71	71	71	71	71	71	71	71	71	71	71	70.5	70.5	70	70	69.5	69.5	69.5	69.5
56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAY59296 standard; peptide; 135 AA. **AAY**59296

AAY59296;

19-APR-2000 (first entry)

Prostate disease marker UC Band #28 amino acid sequence.

Nucleic acid marker; biomarker; tumour; prostate cancer; bladder cancer; benign prostatic hyperplasia; BPH; breast cancer; human; immunodetection

Ното варіелв.

WO9964631-A1

16-DEC-1999.

99WO-US013151. 11-JUN-1999; 98US-00097199 12-JUN-1998;

(UROC-) UROCOR INC.

Veltri RW; Ralph D, O'hara SM, An G,

WPI; 2000-116557/10. N-PSDB; AAZ87584.

Novel RNA biomarkers for diagnosis, prognosis and management of prostate, breast and bladder cancer.

Example 5; Page 184-186; 191pp; English.

The invention provides nucleic acid markers of prostate, breast and bladder cancer. The markers are indicators of malignant transformation of prostate, breast and bladder tissues and are diagnostic of the potential for metastatic spread of malignant prostate timmours. The nucleic acid can also be used as targets for therapeutic intervention in prostate cancer, benign prostatic hyperplasia (BPH), bladder cancer or breast cancer. The markers may be used to design specific probes and primers, for the rapid analysis of prostate, bladder or breast biopsy samples. The probes and primers may also be used for in situ hybridization or in situ PCR detection and diagnosis. They may also be used to identify and isolate full length gene sequences form various DNA libraries. Antibodies against the polypeptide products of the markers can be used to treat prostate cancer, bladder cancer or breast cancer. The encoded proteins may be used

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2001-289849/30.
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                                                                              Sequence 135 AA;
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11-JAN-1996;
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to detect antibodies. The proteins and antibodies can be used in
famunodetection methods for detecting or quantifying the cancers, and for
clinical diagnosis of these cancers. The antibodies may also be used for
radioimaging to quantify and localize the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid marker; biomarker; tumour; prostate cancer; bladder cancer; benign prostatic hyperplasia; BPH; breast cancer; human; immunodetection
                                                                                                                                                                                                                               MRAFLRNQKYEDMENIIHILQIRKLRHRLSNFPRLPGILAPETVLLPFCYKVFRKKEKVK
                                                                                                                                                                                                         1 MRAFLRNQKYEDMHNIIHILQIRKLRHRLSNFPRLPGILAPETVLLPFCYKVFRKKEKVK
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                                                                                                                                                                      Gaps
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                                                                                                                               100.0%; Score 694; DB 3; Length 135; 100.0%; Pred. No. 6.9e-75; ive 0; Mismatches 0; Indels
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N-PSDB; AAZ87583.
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                                                                                                                                                Local Similarity
                                                                                             Sequence 135 AA;
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                                                                                                                                 Query Match
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The sequence represents the amino acid sequence of biomarker protein encoded by UC band 28 #2. Proteins encoded by the nucleic acid markers and be used to produce antibodies for the detection of prostate. breast or bladder cancer. Blomarker nucleic acid sequences can be used as hybridisation probes and primers that specifically hybridise to prostate cancer, benign prostatic hyperplasia (BFH), bladder cancer or breast cancer markers. The nucleic acids can be used as targets for therapeutic intervention in these diseases, in the identification and isolation of full-length gene sequences, including regulatory elements for gene full-length deman DNA libraries, as hybridisation probes for screening genomic human DNA libraries. The kits comprising the nucleic acid sequences are useful for detecting bladder, breast or prostate
immunodetection methods for detecting or quantifying the cancers, and for clinical diagnosis of these cancers. The antibodies may also be used for radioimaging to quantify and localize the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MRAFLRNOKYEDMHNIIHILOIRKLRHRLSNFPRLPGILAPETVLLPFCYKVFRKKEKVK
                                                                                                                                                                                                                                                                                                                                                                                1 MRAFLRNOKYEDMHNIIHILQIRKLRHRLSNFPRLPGILAPETVLLPFCYKVFRKKEKVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prostate; breast; bladder; cancer; biomarker; probe; diagnostic; benign prostatic hyperplasia; BPH; therapeutic; human.
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100.0%; Pred. No. 6.9e-75;
ive 0; Mismatches 0;
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96US-0013611P.
96US-00692787.
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Best Local Similarity 100.
Matches 135; Conservative
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Length 135;

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Sequence 135 AA;
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                                                                                                                                          61 RSQKATEFIDYSIEQSHHAILTPLQTHLTMKGSSMKCSSLSSEAILFTLTLQLTQTLGLE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acids as biomarkers and targets useful for detecting, diagnosing, prognosing, and in developing treatments for prostate, breast and bladder cancer.
                                                                                              9
                                                                                                         Biomarker protein encoded by UC band 28 #3, used in diagnosis of cancer.
                                                                                          1 MRAFLRNQKYEDMHNIHILQIRKLRHRLSNFPRLPGILAPETVLLPFCYKVFRKKEKVK
                                                                      Gaps
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                                             100.0%; Score 694; DB 4; Length 135; 100.0%; Pred. No. 6.9e-75; ive 0; Mismatches 0; Indels
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cancer cells in a biological sample
cancer cells in a biological sample
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96US-0013611P.
96US-00692787.
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31-JUL-1996;
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The invention provides nucleic acid markers of prostate, breast and bladder cancer. The markers are indicators of malignant transformation of prostate, breast and bladder tissues and are diagnostic of the potential for metastatic spread of malignant prostate tumours. The nucleic acid can also be used as targets for therapoutic intervention in prostate cancer, benign prostatic hyperplasia (BPH), bladder cancer or breast cancer. The markers may be used to design specific probes and primers, for the rapid primers may also be used for in situ hybridization or in situ PCR detection and diagnosis. They may also be used to identify and isolate till length gene sequences form various DNA libraries. Antibodies against the polypeptide products of the markers can be used to treat prostate cancer, bladder cancer or breast cancer. The encoded proteins may be used to detect antibodies. The proteins and antibodies can be used in immunodetection methods for detecting or quantifying the cancers, and for climical diagnosis of these cancers. The encoded proteins may be used to triand diagnosis of these cancers. The encoded proteins may be used to climical diagnosis of these cancers. The encoded proteins may be used for radioimaging to quantify and localize the encoded proteins
                                                                                                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                                                                                          61 RSQKATEFIDYSIEQSHHAILTPLQTHLIMKGSSMKCSSLSSEAILFTLTLQLTQTLGLE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid marker; biomarker; tumour; prostate cancer; bladder cancer; benign prostatic hyperplasia; BPH; breast cancer; human; immunodetection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel RNA biomarkers for diagnosis, prognosis and management of prostate,
                                                                                                                                                             9
                                                                                                                                                                                                                                     9
                                                                                                                                                                                                     1 MRAFLRNOKYEDMANIIHILOIRKURHRLSNFPRLPGILAPETVLLPFCYKVFRKKEKVK
                                                                                                                                                                                                                                                                                                                  RSQKATEFIDYSIEQSHHAILTPLQTHLTMKGSSMKCSSLSSEAILFTLTLQLTQTLGLE
                                                                                                                                                             1 MRAFLRNOKYEDMHNIIHILQIRKLRHRLSNFPRLPGILAPETVLLPFCYKVFRKKEKVK
                                                                                Gaps
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                                                                                Indels
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100.0%; Score 694; DB 4;
100.0%; Pred. No. 6.9e-75;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cancer biomarker UC28 antigenic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Veltri RW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY59294 standard; peptide; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US013151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCLLYLSKTIHPOII 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-00097199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CCLLYLSKTIHPQII 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O'hara SM, Ralph D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           breast and bladder cancer.
Query Match
Best Local Similarity 100.1
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .9-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-116557/10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9964631-A1
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(first entry)

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cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; barnce; plant disease realstance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate;
                                                                                     Recombinant DNA construct; transformed plant; improved plant property;
                                                                                                                                                  nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
bacterial polypeptide.
                                                            Bacterial polypeptide #20398.
                                                                                                                                                                                                             US2003233675-A1.
                                    02-DEC-2004
            ADS41968;
                                                                                                                                                                                      Bacteria.
 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents the amino acid sequence of biomarker, UC band 28, antigenic peptide used to produce antibodies for the detection of prostate. Decast or bleader cancer. Biomarker nucleic acid sequences can be used as hybridisation probes and primars that specifically hybridise to prostate cancer, benign prostatic hyperplasia (BPH), bladder cancer or breast cancer markers. The nucleic acids can be used as targets for therepeutic intervention in these diseases, in the identification and isolation of full-length gene sequences, including regulatory elements for gene expression, from genomic human DNA libraries, as hybridisation probes for screening genomic human DNA libraries. The kits comprising the nucleic acid sequences are useful for detecting bladder, breast or prostate cancer cells in a biological sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acids as biomarkers and targets useful for detecting, diagnosing, prognosing, and in developing treatments for prostate, breast and bladder cancer.
                        Gaps
                                                                                                                                                                                                           Biomarker UC band 28, antigenic peptide used in diagnosis of cancer.
                                                                                                                                                                                                                                   Prostate; breast; bladder; cancer; biomarker; probe; diagnostic; benign prostatic hyperplasia; BPH; therapeutic; human; antigenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 21;
14.8%; Score 103; DB 3; Length 21;
                       0; Indels
          5.7e-05;
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Pred. No. 5.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.8%; Scor.
100.0%; Pred. No. ...
'... 0; Mismatches
          Best Local Similarity 100.0%; Pred. No. 5.7
Matches 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 O'hara SM, Ralph D, Veltri R;
                                                                                                                                     AAU02173 standard; peptide; 21 AA.
                                               54 RKKEKVKRSQKATEFIDYSIE 74
                                                              1 RKKEKVKRSQKATEFIDYSIE 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Col 73; 78pp; English
                                                                                                                                                                                                                                                                                                                                                                       95US-0001655P.
96US-0013611P.
96US-00692787.
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                                                                                                                                                                                   (first entry)
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21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-289849/30.
                                                                                                                                                                                                                                                                                                                                                                                                                         (UROC-) UROCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21 AA;
                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                US6218529-B1
                                                                                                                                                                                                                                                                                                                                                 12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                       31-JUL-1995;
11-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                 31-JUL-1996;
                                                                                                                                                                                   29-AUG-2001
                                                                                                                                                                                                                                                                                                                        17-APR-2001
                                                                                                                                                            AAU02173;
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Best Local S
Query Match
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Matches
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to promoter favoresaion of a polymucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant transformed plant an improved property comprises transforming a plant second plant having an improved property comprises transformed plant where the recombinant DNA construct and growing the transformed plant where the copolinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regularors, increased rate of homologous recombination, modified seed oil or protein yield and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant DNA construct comprising a promoter positioned to provide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphorus use and/or upcake, by modification of photosynchesis or by providing improved plant growth and development under at least one stress condition, improved lighth production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---RLPGILAPETVLLPFCYKVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     content, improved yield by modification of carbohydrate, nitrogen or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     format from USPTO at seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goldman BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 20398; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 MHNIHILQIRKLRHRL----SNFP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Slater SC,
                                                                       20-FEB-2003; 2003US-00369493.
                                                                                                                                                  21-FEB-2002; 2002US-0360039P.
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Best Local Similarity 26.84
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-061375/06.
                                                                                                                                                                                                                                                                                                                                                                               GOLDMAN B S.
                                                                                                                                                                                                                                                                HINKLE G J.
SLATER S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hinkle GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 371 AA;
                                                                                                                                                                                                                                                                                                                                           CHEN X
                                                                                                                                                                                                                             CAO
18-DEC-2003.
                                                                                                                                                                                                                                                                                                                                       (CHEN/)
                                                                                                                                                                                                                     (CAOY/)
                                                                                                                                                                                                                                                                    HINK/)
                                                                                                                                                                                                                                                                                                    (SLAT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
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Gaps

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0; Indels

ADS41968 ID ADS41968 standard; protein; 371 AA.

RESULT 7

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to promoter for expression of a polymucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and method of producing a transformed plant encombinant property comprises transformed plant with the avoing an improved property comprises transformed plant with the recombinant DNA construct and growing the transformed plant, where the recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, tincreased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                            1 NLTYGLKSSEELNEFLKDFDIHSHHA-FTPLSLKALKAGKOMEKGTLLTTHSISFAHES 129
                                                  54 RKKEKVKRSQKATEFI-DYSIEQSHHAILTPLQTHLTMKGSSM-KCSSLSSEAILFTLTL 111
                                                                                                                                                                                                                                                                                                                                                                                                                           cold tolerance; heat tolerance; drought tolerance; herbicide; formosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
Goldman BS;
                                                                                                                                                                                                                                                                                                                                                                                                             construct; transformed plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 1334; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen X,
                                                                                                                                                                                                                                                       ADN18681 standard; protein; 381 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Slater SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-FEB-2002; 2002US-0360039P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-FEB-2003; 2003US-00369493
                                                                                                                                                                                                                                                                                                                                                                      Bacterial polypeptide #1334
                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                            112 OLTOTIG 118
                                                                                                                                                             130 KLWDTLG 136
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SLATER S C.
CHEN X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-061375/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hinkle GJ,
                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant DNA
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                                                                                                                                                                                                                                                                                                                                 02-DEC-2004
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                                                                                                                                                                                                                                                                                              ADN18681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SLAT/)
(CHEN/)
(GOLD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAOY/)
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                                                                                                                                                                                                                    RESULT
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            providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                      54 RKKEKVKRSQKATEFI-DYSIEQSHHAILTPLQTHLTMKGSSM-KCSSLSSEAILFTLTL 111
                                                                                                                                                                                                                                               23
                                                                                                                                                                                                                                                                               73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to identifying target proteins (ABB90790-ABB94016)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                24 MHNL--AIKLRERGHEVGIVTNNRPTGKEELKRYGIELIKIPGIISP------FLDV
                                                                                                                                                                                                                                             -----RLPGILAPETVLLPFCYKVF
phosphorus use and/or uptake, by modification of photosynthesis or by
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                            32;
                                                                                                                                                                       ; Score 90; DB 8; Length 381;
; Pred. No. 0.11;
23; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; SEQ ID NO 54; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herbicidally active polypeptide SEQ ID NO 54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                                                                             13 MHNIIHILQIRKLRHRL----SNFP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB90843 standard; protein; 645 AA.
                                                                                                                                                                         13.0%;
26.8%;
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                                                                                                                                                                                                         34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                         133 KLWDTLG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-269010/31.
                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          OLTOTIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (FARB ) BAYER AG.
                                                                                                                                          Sequence 381 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200210210-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                        112
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                                                                                                                                                                                                         Matches
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Sequence 645 AA;

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                                                                 Sequence 384 AA;
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                                                                                                                           Query Match
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                                                                                                                                                                                             Matches
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It ransformation, and homologous recombination. The genome is preferably the genome of a hyperthermostable archaebacterium, particularly Thermococcus kodakaraensis KODI. The method is for targeting the Gisruption of a gene in the genome of an organism, which is applicable in grudying gene structure and functions as well as enzyme activities of encoded proteins and useful in medicine, forensic science food or drug inspection, molecular blology and immunology, with this method, the disruption of a gene at an arbitrary position in a genome can be achieved efficiently and reliably. The present sequence is that of a protein encoded by the genome of Thermococcus kodakaraensis which was derived using the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained
                                                                                              5,
                                                                                                                                                                                                                                                                                                                     99 MIHLLAGFIYGPHWPWVMIAVIVFKMLIGIVSFLIALSLVTLLPLLLKA--KVREFMLSK 156
                                                                                                                                                                                                                                                                                     64 KATEFIDYSIEQSHHAILTPLQTHLTMKGSSMKC-SSLSSEAILFTLTLQLTQTLGLECC 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Method for disrupting targeted gene in genome of organism particularly thermostable bacterium and with genome chips for analysis, applicable in studying gene structure and functions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene disruption; gene targeting; marker gene; transformation; homologous recombination; hyperthermostable archaebacterium; KOD1; gene structure; gene function; enzyme activity; medicine; forensic science; food; drug inspection; molecular biology; immunology.
                                                                                                                                                            -----LLPFCYKVFRKKEKVKRSQ
                                                                                              Gaps
                                                                                           29;
                                   Length 645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermococcus kodakaraensis KOD1 protein sequence SeqID1977.
                                                                                              46; Indels
                                Query Match 11.9%; Score 82.5; DB 5; Best Local Similarity 23.5%; Pred. No. 1.7; Matches 31; Conservative 26; Mismatches 46;
                                                                                                                                                         25 LRHRLSNF---PRLPGILAPETV------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermococcus kodakaraensis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 AVWIPNEIKTEM 223
                                                                                                                                                                                                                                                                                                                                                                                                             123 LLYLSKTIHPQI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Imanaka T, Atomi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-257583/24.
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in electronic format directly from WIPO at

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This invention relates to novel PFM (PR family member)/SET (Su(var)3-9, Enhancer-of-Zeste and Trithorax) nucleotides and encoded polypeptides thereof that are implicated in proliferative disorders such as cancer. Specifically, it refers to a functional fragment of the PFM/SET tumour suppressor gene that encodes a PR, SET, PRAZ or PKZL domain. The present invention describes the identification and characterisation of additional PR/SET-domain family members that can be used as regulators of cell proliferation and furthermore to treat, prevent or diagnose hyperproliferative disorders including scleroderma, arthritis, alcoholic
                                                                                                                                                                                                                                                                                                                                   54 RKKEKVKRSQKATEF-IDYSIEQSHHAILTPLQTHLTMKGSSM-KCSSLSSEAILFTLTL 111
                                                                                                                                                                                                                                                                                                                                                                                     23
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arthritis, keloids, atherosclerosis, Huntington's disease or Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alzheimer's disease; paralysis; cerebellar atrophy; cytostatic;
neuroprotective; nootropic; antiarthritic; vulnerary;
antiatherosclerotic; antidiabetic; hepatotropic; PFM; PR family member.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New PR/SET-domain containing nucleic acids (which encodes PFM/SET) and
                                                                                                                                                                       ---NFPRLPGILAPETVLLPFCYKVF
                                                                                                                                                                                                                 1 :: | | | : | | : | | : | | : | | : | | : | | : | | : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorder; scleroderma;
                                                                                            Gaps
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                                                                                        32;
            Length 384;
                                                                                        42; Indels
            DB 8;
11.7%; Score 81; DB 8
23.3%; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human PFM7 protein, a PR/SET family member.
                                                                                        28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 21; SEQ ID NO 4; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADF50279 standard; protein; 1061 AA.
                                                                                                                                                                       13 MHNIIHILQIRKLRHRLS----
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                                                  Local Similarity 23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 QLTQTLGLECCLL 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-FEB-2004 (first entry)
                                                                                        31; Conservative
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                                                                                                                                                                                                                                                                                            60 KR--SQKATEFIDYSIEQSHHAILTPLQTH-LTMKGSSMKCSSLSSEAILFTLTL---- 111
liver cirrhosis, hypertropic scarring and atherosclerosis. Through gene therapy, these polymucleotides can be used to enhance proliferation of normal cells without rendering the cells cancerous and as such they are particularly useful for treating buchenne's muscular dystrophy, insulindependent diabetes mellitus, Huntington's, Parkinson's, Alzheimer's compositions can be described as cytostatic, neuroprotective, nootropic, antiatheristic, vulnerary, antiatherosclerotic, antidiabetic or hepatotropic. This polypeptide sequence is the human PFM7 protein (encoded by a PFM/SET gene localised to chromosome 11q25) of the
                                                                                                                                                                                                                                        18 HILO-----IRKLR------HRLSNFPRLPGILAPETVLLPFCYKVFRKKEKV
                                                                                                                                                                                                               31; Gaps
                                                                                                                                                                                     Query Match 11.2%; Score 77.5; DB 7; Length 1061; Best Local Similarity 28.6%; Pred. No. 13; Matches 36; Conservative 17; Mismatches 42; Indels 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADO36741 standard; protein; 1061 AA
                                                                                                                                                                                                                                                                                                                                                112 QLTQTL 117
                                                                                                                                                                                                                                                                                                                                                                          819 ELSQTL 824
                                                                                                                                                              Sequence 1061 AA;
                                                                                                                                      nvention.
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comprising the vector; an oligonucleotide comprising at least 17 contiguous nucleotides of the nucleic acid molecule; a primer pair for detecting PFM/SET nucleic acid molecule; a primer pair for detecting PFM/SET nucleic acid molecule in a sample; coligonucleotides; detecting PFM/SET nucleic acid molecule in a sample; modulating cell growth by introducing the vector into a host cell, and expressing the encoded PFM/SET polypeptide in a mamount effective to modulate growth of the cell; isolating PFM/SET polypeptide by growing the polypeptide; the isolated PFM/SET polypeptide, or its functional fragment; an isolated immunogenic PFM/SET polypeptide, or its functional fragment; an isolated immunogenic PFM/SET polypeptide, comprising at least 8 contiguous amino acids of PL-P9; an antibody or its antigen-binding fragment that specifically binds to PFM/SET polypeptide in a sample; and screening for a compound that contacting the polypeptide with one or more candidate compounds, and determining histone methyltransferase activity by contacting the polypeptide with one or more candidate compounds, and determining histone methyltransferase activity of the contacted useful for diagnosing, prognosing, preventing and treating proliferative disorders, e.g. cancer. This is the amino acid sequence of PR-domain

9

Gaps

42; Indels 31; DB 8; Length 1061;

Best Local Similarity

Query Match

Sequence 1061 AA;

763

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60 KR--SQKATEFIDYSIEQSHHAILTPLQTH-LTMKGSSMKCSSLSSEAILFTLTL---- 111
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                                                                                                                                                                     18 HILQ------IRKLR-----HRLSNPPRLPGILAPETVILPFCYKVFRKKEKV
                                                                                                                                                                                                                                             704 HILKNHPGAELPPSIRKLRPAGPGEPDPMLSTHTQLTGTIATPPVCCPHCSKQYSSKTKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila, developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster polypeptide SEQ ID NO 1164.
11.2%; Score 77.5; DE 28.6%; Pred. No. 13; ive 17; Mismatches
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11-JUL-2000; 2000US-00614150.
                                                                                        36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 QLTQTL 117
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ELSQTL 824
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                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFM/SET polypeptide, useful for diagnosing, prognosing, preventing and treating proliferative disorders, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFM/SET protein binding motif; cell growth modulator;
histone methyltransferase activity; proliferative disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid molecule comprising a sequence encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               methyltransferase; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human PR-domain containing protein PFM-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 4; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUL-2002; 2002US-0020012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .8-JUL-2002; 2002US-00200012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; histone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-121568/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PR-domain; PFM-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2004014192-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUAN/) HUANG S.
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Homo sapiens.

22-JAN-2004

Huang S;

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cc of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as given in the specification. Also described are: a recombinant expression vector; a cell comprising a recombinant expression vector; a cell comprising a recombinant expression ucleic acid comprising an ucleotide sequence of at least 8 nucleotides in length; a vaccine composition for prevention or treatment of an S. epidermidis infection, comprising a nucleic acid cited above and a carrier; treating infection, comprising a nucleic acid cited above and a carrier; treating ca subject for S. epidermidis infection; a recombinant or substantially pure preparation of an S. epidermidis polypeptide or its fragment; a vaccine composition for prevention or treatment of an S. epidermidis infection; detecting the presence of a Staphylococcus mucleic acid in a sample; a computer readable medium having recorded in it the nucleotide sequences with SEQ ID NO: 1-3772 or its fragments; a computer based system for identifying fragments of the Staphylococcus genome of commercial importance; a computer based system for identifying consensually important nucleic acid fragments of the Staphylococcus spanements of the Staphylococcus genome and/or plasmids; and identifying an expression modulating fragment commercially important invention are useful for the diagnosis, prevention and/or treatment of an Staphylococcal epidermidis bacterial infection. This is the amino acid sequence of a S. epidermids protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 NQXYED-MHNIHILQIR-----KLRHRLSNFPRLPGILAPETVL----LPFCYKV 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 FRKKEKVKR---SQKATEFIDYSIEQSHHAI-------LTPLQTHLTMKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSMKCSSLSSEA-----ILFTLTLQLTQTLGLECCLLYLSKTIHPQII 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.1%; Score 77; DB 8; Length 1026; 20.6%; Pred. No. 15; 21ve 33; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Photorhabdus luminescens protein sequence #2140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Taourit S, Glaser P, Frangeul L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABM69043 standard; protein; 322 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-FEB-2001; 2001FR-00001659.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 20.6*
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Photorhabdus luminescens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1026 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       whooping cough.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200294867-A2.
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Buchrieser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABM69043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABM69043
                   %%GGGGGGGGGGGGGGGGGGGGGGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
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                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB5737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     718 NOVHELQ-RKLRHVSSNL------KAIDLPINFKFFFLKTDRHGQEKAK--SQIQKF 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes an isolated nucleic acid comprising a nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis; recombinant expression vector; infection; computer readable medium; computer based system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 NIHHILQIRKLRHRLSNFPRLPGILAPETVLLPFCYKVFRKK-----EKVKRSQKATEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polypeptide and encoding nucleic acid derived from Staphylococcus epidermidis, useful for diagnosing, preventing and/or treating an S. epidermidis bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25;
                                                                                          Disclosure; SEQ ID NO 1164; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.2%; Score 77.5; DB 4; Length 1144; 30.0%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 IDYSIEQSH-----HAILTPLQTHLTMKGSSMKCSSLS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               766 INFILEDDHINGSEAIYTFLSPSSDHLKQSLPSPKKSKFS 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus epidermis polypeptide seqid 7479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; SEQ ID NO 7479; 741pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADS08184 standard; protein; 1026 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2003; 2003US-00724972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-00134001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Doucette-Stamm L, Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 30.0
nes 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-580138/56.
N-PSDB; ADS04412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2004147734-A1.
                   interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-NOV-2004
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Matches

셤 ò 셤

£X8X00000000000X8

ADS08184

92

Danchin A;

Kunst F,

48; Gaps

WPI; 2003-148459/14.

Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides.

The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are proteins from Photorhabdus luminescens. The isolated sequences are courses of probes and primers for detecting the genome of P. luminescens and related species, to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the CD lypeptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that companials or microcorganisms other than P. luminescens and each be to alter response or sensitivity to toxins and antibiotics produced by P. companials or microcorganisms other than P. luminescens and Ab are also useful for recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The companiant vector containing the genes and Ab are also useful charapeutically (to treat microbial infection by bacteria or fungilate and sensitive to P. luminescens-encoded toxins or antibiotics) and as CC factors and for identifying targets of human diseases for which P. CC luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens Claim 2; SEQ ID NO 2140; 1205pp; French

Sequence 322 AA;

tch al Similarity 26.6%; Pred. No. 3.5; DB 6; Length 322; al Similarity 26.6%; Pred. No. 3.5; 29; Conservative 19; Mismatches 50; Indels 11; Gaps Query Match Best Local Similarity Matches 29; Conserva

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13 MANIIHILQIRKIRHRISNPPRIPGILAPETVLIPFCYKVFRKKEKVKRSQKATEFIDYS 72

73 IEOSHHAILTPLOTHLTM-KGSSM--KCSSLSSEAILFTLTLQLTQTLG 118

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ઠે 셤 273 PDENINRIVASWPGHPDISRGLSLGFHADNTFSDTIRAFITNNLSQTGG 321

Search completed: September 9, 2005, 13:00:51 Job time: 62.5 secs

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99, Appl
2, Appli
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Sequence 86, Appl
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                                                      September 9, 2005, 12:25:33; Search time 17.5 Seconds (without alignments) 575.864 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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| S-09-949-016-9182
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Maximum Match 100%
Listing first 45 summaries
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Match Length DB
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Perfect score:
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Sequence 5446, Ap	US-09-134-001C-5446	m	315	9.3	64.5	45
Sequence 6873, Ap	US-09-107-532A-6873	4	236	9 .3	64.5	44
Sequence 6, Appli	US-09-231-899-6	4	288	9.4	ø	43
Sequence 6, Appl:	US-09-090-793-6	m	288	9.4	65	42
Sequence 9, Appli	US-08-752-929-9	ч	288	9.4	65	41
Sequence 9, Appl:	US-08-375-709-9	н	288	9.4	65	40
4	US-09-270-767-48284	4	258	9.4	65	39
Sequence 33067,	US-09-270-767-33067	4	258	9.4	65	38
Sequence 6155, A	US-09-621-976-6155	4	75	9.4	65	37
Sequence 27, Appl	US-08-764-100-27	-	3218	9.4	65.5	36
	US-09-538-092-151	4	698	9.4	65.5	35
	US-09-949-016-7139	4	611	9.5	99	34
Sequence 856, App	US-09-438-185A-856	4	348	9.5	99	33
	US-09-198-452A-922	4	348	9.5	99	32
Sequence 46386,	US-09-270-767-46386	4	267	9.5	99	31
Sequence 8285, A	US-09-949-016-8285	4	1813	9.6	66.5	30
Sequence 8284, Ap	US-09-949-016-8284	4	1813	9.6	66.5	53
Sequence 8283, A	US-09-949-016-8283	4	1813	9.6	99	28

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MEDIUM TYPE: Floppy
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COUNTRY: USA
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US-09-949-016-9182
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MRAFLRNQKYEDMHNIHHILQIRKLRHRLSNFPRLPGILAPETVLLPFCYKVFRKKEKVK 60
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100.0%; Pred. No. 4.7e-77;
tive 0; Mismatches 0; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,199
FILING DATE:
CLASSIETCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/692,787
FILING DATE: 31-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Nakashima, Richard A.
REGISTATION NUMBER: P-42,023
REFERENCE/DOCKET NUMBER: P-42,023
TELECOMMUNICATION INFORMATION:
TELEPRATION SECUENCE J3000
TELEPRAX: (512) 418-3000
TELEPRAX: (512) 414-7577
INFORMATION FOR EQUID NO: 86:
SEQUENCE CHRACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acids
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MEDIUM TYPE: Floppy disk
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Matches 135, Conservative
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| cgn2 6/ptodata/2/pubpaa/USO6 MW PUB.ppp:*
| cgn2 6/ptodata/2/pubpaa/USO6 PUBCOMB.ppp:*
| cgn2 6/ptodata/2/pubpaa/USO7 NEW PUB.ppp:*
| cgn2 6/ptodata/2/pubpaa/USO7 NEW PUB.ppp:*
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| cgn2 6/ptodata/2/pubpaa/USO0 PUBCOMB.ppp:*
| cgn2 6/ptodata/2/pubpaa/USO0 NEW PUB.ppp:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1777461 seqs, 394431504 residues
                                                                                                                                                                                                                                           9, 2005, 12:59:09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                         US-09-974-546C-84
                                                                                                                                                                                                                                       September
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
Sequence:
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                                                                                                                                                                                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

tion	nce 84, Appl nce 86, Appl nce 26, Appl nce 2039, A nce 13297, nce 174106, nce 324095, nce 324095, nce 324095,
Description	Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence
SUMMARIES	US-09-974-546-84 US-09-974-546-86 US-09-974-546-86 US-09-974-546-86 US-10-369-493-1334 US-10-425-115-324095 US-10-425-115-324095 US-10-425-115-324095 US-10-425-115-324095
89	10 10 10 115 116 116 116
* Query e Match Length DB 1	135 135 135 135 1478 1478 1444 1444 1289
& Query Match	1000.0 1000.0 13.0 13.0 111.7 111.1 11.2
Score	694 694 103 90 90 91 79 79 79
Result No.	1106480CB001

Sequence 4, Appli Sequence 7479, Ap	Sequence	Sequence 70203	Sequence 32412	Sequence 32412			Sequence	Sequence 36299	Seguence	Sequence 32410	Seguence	Seguence	Sequence		Seguence	Seguence	Seguence 6988;	Seguence	Sequence 2678		24307		'n	Sequence 2, Appli	6 8	7	7	Sequence 2647	N	Sequence 1696	Sequence 1259	Sequence 63743, A
15 US-10-200-012-4	US-10-425-	_		US-1	US-10-424-59		US-10-425-11	16 US-10-425-115-362998		US-10-425-115	1	US-10-425-115	16 US-10-425-115-238564	16 US-10-425-115-324099	US-10-739-930	US-10-424-599	15 US-10-425-114-69882	16 US-10-425-115-327356	US-10-424-599	US-10-425-114	US-10-425-115-2430	-238	16 US-10-425-115-324123	9 US-09-866-557A-2	11 US-09-858-862-2	us-	US-10-350-798	US-10-424-599	17 US-10-876-086-27	US-10-408-765	-10-437-963	15 US-10-425-114-63743
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11.2	11:1	10.8	10.8	10.8	10.7	10.7	10.7	10.7	10.7	10.7	10.7	10.7	10.5	10.5	10.4	10.4	10.3	10.3	10.3	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.1	10.1	10.1
77.5	77	75	75	75	74.5	74.5	74	74	74	74	74	74	73	73	72.5	72	71.5	71.5	71.5	71	71	71	71	71	71	71	71	70.5	70.5	70	70	70
12	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Sequence 84, Application US/09974546

Publication No. US20030050470A1

GENERAL INFORMATION:

APPLICANT: An, Gang
O'Hara, S. Mark
Ralph, David
Veltri, Robert
TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
BROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
NUMBER OF SEQUENCES: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NDRER: US/09/974,546
FILING DATE: 10-Oct-2001
CLASSIFICATION: Unknown
                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/097,199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1998-06-12
ATTORNEY/AGENT INFORMATION:
NAME: Nakashima. Richad A.
REGISTRATION NUMBER: P-42,023
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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ZIP: 77210
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US-09-974-546-84
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US-09-974-546-56
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                                                                                                                                                                                                                                                                                                                                                                                                                      1 MRAFLRNOKYEDMINIIHILQIRKLRHRLSNFPRLPGILAPETVLLPFCYKVFRKKEKVK 60
                                                                                                                                                                                                                                                                                                                                                                               1 MRAFLRNOKYEDMHNIIHILQIRKLRHRLSNFPRLPGILAPETVLLPFCYKVFRKKEKVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 86, Application US/09974546
Publication No. US20030050470A1
GRNERAL INFORMATION:
APPLICANT: An, Gang
O'Hara, S. Mark
Ralph, David
Veltri, Robert
Veltri, Robert
PROGNOSIS AND TARGETS FOR DIAGNOSIS,
PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                        Length 135;
                                                                                                                                                                                                                                                                                                                                    Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
COMPUTER: TBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/974,546
FILING DATE: 10-Oct-2001
CLASSIFICATION: UNKNOWN
                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 694; DB 10;
Best Local Similarity 100.0%; Pred. No. 9.1e-72;
Matches 135; Conservative 0; Mismatches 0;
                                    TELEPHONE: (512) 418-3000
TELEFAK: (512) 474-7577
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 84:
REFERENCE/DOCKET NUMBER: UROC:018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Nakashima, Richard A.
REGISTRATION NUMBER: P-42,023
REFERENCE/DOCKET NUMBER: UROC:018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/097,199
FILING DATE: 1998-06-12
ATTORNEY/AGENT INFORMATION:
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TELEPHONE: (512) 418-3000
TELEPAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
                    TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CCLLYLSKTIHPQII 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Texas
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
US-09-974-546-86
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                                                                                                                                                                                                                                1 MRAFLRNQKYEDMHNIHILQIRKLRHRLSNFPRLPGILAPBTVLLPFCYKVFRKKEKVK 60
                                                                                                                                                                                                    1 MRAFLRNOKYEDMHNIIHILQIRKLRHRLSNFPRLPGILAPETVLLPFCYKVFRKKEKVK
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 56, Application US/09974546
Publication No. US20030050470A1
GENERAL INFORMATION:
APPLICANT: An, Gang
O'Hara, S. Mark
Ralph, David
Veltri, Robert
TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                    Length 135;
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                                                                                                                                                   Indels
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                  Query Match 100.0%; Score 694; DB 10; Best Local Similarity 100.0%; Pred. No. 9.1e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 14.8%; Score 103; DB 10;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 21; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/974,546
FILING DATE: 10-Oct-2001
CLASSIFICATION: Unknown
PRIOR APPLICATION: Unknown
APPLICATION DATA:
APPLICATION NUMBER: 09/097,199
FILING DATE: 1998-06-12
ATTORNEY/AGENT INFORMATION:
NAME: NAKASHAINA:
REGISTRATION NUMBER: P-42,023
                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: UROC:018 TELECOMMUNICATION INFORMATION:
) MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-09-974-546-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 RKKEKVKRSQKATEFIDYSIE 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                          121 CCLLYLSKTIHPOII 135
                                                                                                                                                                                                                                                                                                                                                                                                      121 CCLLYLSKTIHPQII 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 77210
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 87
                                                                                                                                                   Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
```

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

September 9, 2005, 13:01:39; Search time 14.5 Seconds Run on:

(without alignments) 895.811 Million cell updates/sec

1 MRAFLRNQKYEDMHNIHIL......TLGLECCLLYLSKTIHPQII 135 US-09-974-546C-84 694 Title: Perfect score:

BLOSUM62 Scoring table:

Sequence:

283416 seqs, 96216763 residues Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STEMMARTES

		*			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ΙD	Description
-	06	13.0	381	7	F71196	probable hexosyltr
7	82.5	11.9		~	F86174	hypothetical prote
m	80	11.5		Н	MNXRSA	nonstructural prot
4	78.5	11.3	m	N	T21328	hypothetical prote
S	78	11.2		~	D64555	conserved hypothet
9	74.5	10.7		~	A58456	X protein - human
7	74.5	10.7	263	7	A82069	hypothetical prote
80	72.5	10.4	196	~	T43782	hypothetical prote
σ	71.5	10.3	227	~	B84040	ABC transporter (A
10	71.5	10.3	451	~	D70045	two-component sens
11	70.5	10.2	_	~	T40751	isoleucyl-trna syn
12	70	10.1		~	T06761	hypothetical prote
13	70	10.1			A44831	phosphoenolpyruvat
14	70	10.1		7	AE2413	phosphoenolpyruvat
15	69.5	10.0	1398	~	H71606	hypothetical prote
16	69	9.9	154	~	T27983	hypothetical prote
17	69	9.9	743	7	T00634	hypothetical prote
18	69	9.9	1850	~	AC1917	serine/threonine k
19	68.5	9.9	503	-	S11338	steroid 11beta-mon
20	68.5	9.9	2470	~	S57085	1-phosphatidylinos
21	68	9.8	379	~	C75006	hypothetical prote
22	68	9.6	414	Н	H64203	histidine-tRNA lig
23		9.8	496	~	A31986	glucose transporte
24		9.8	639	~	T13151	adapter protein CM
25	68	9.8	5126	0	S40450	ryanodine receptor
56	67.5	9.7	619	~	B87682	hypothetical prote
27	67.5	9.7	833	~	T28385	ORF MSV224 probabl
28	67.5	9.7	1278	~	A71609	probable secreted
53	67.5	9.7	3225	~	D81702	adherence factor T

hypothetical prote hypothetical prote hypothetical prote translation initia protein kinase Dar	hypothetical prote precorrin-2 C20-me hypothetical prote ethylene receptor DNA mismatch repai	hypothetical prote tuberous sclerosis outer membrane pro major outer membra transcription fact probable Fe-S oxid
T03757 E96506 B82440 T01452 A54099	S37927 AC3341 T21716 T06537 H70327	T22376 A49420 D86597 H72027 A42029 F97147
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126 213 317 347 517	587 244 635 859	908 1784 344 344 446 472
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SSULT	71196

probable hexosyltransferase (EC 2.4.1.-) PH1844 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: F71196
R;Kawarabayasi, Y:; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
M.; Res. 5. 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic and A;Status: P71196
A;Status: P71196
A;Status: P71196
A;Status: P71196
A;Status: J.381 **KAW*
A;Rocession P71196
A;Status: J.381 **KAW*
A;Rocession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Genetics:
A;G

Gaps 32; DB 2; Length 381; 38; Indels Query Match 13.0%; Score 90; DB 2; Best Local Similarity 26.8%; Pred. No. 0.16; Matches 34; Conservative 23; Mismatches

7

13 MHNIIHILQIRKLRHRL---SNFP----SNFP-53

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73 24 MHNL--AIKLRERGHEVGIVTNNRPTGKEEELKRYGIELIKIPGIISP------FLDV 셤 셤

54 RKKEKVKRSQKATEFI-DYSIEQSHHAILTPLQTHLTMKGSSM-KCSSLSSEAILFTLTL 111

112 QLTQTLG 118 ઠે

133 KLWDŤĽG 139

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RESULT 2 F86174

hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: O-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: F86174
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, E.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

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Query Match
Best Local Similarity
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A; Residues: 1-172 <ZEN>
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NyAlternate names: nonstructural protein NS53
C;Species: simian rotavirus SAll
C;Decies: simian rotavirus SAll
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: S08215
R;Mitchell, D.B.; Both, G.W.
A;Title: Conservation of a potential metal binding motif despite extensive sequence dive
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A;Molecule type: genomic RNA
A;Residues: 1-495 <MIT>
A;Cross-references: UNIPROT:P15687; EMBL:X14914; NID:g61889; PIDN:CAA33039.1; PID:g61890
C;Genetics:
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A;Resduces: 1-645 <STO>
A;Cross-references: UNIPROT:P93825; GB:AE005172; NID:g2341041; PIDN:AAB70445.1; GSPDB:GN C;Genetics:
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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T21328
hypothetical protein F25C8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21328
R;Matchtews, L.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19407
A;Accession: T21328
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                         ----LLPFCYKVFRKKEKVKRSQ
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C;Superfamily: bovine rotavirus nonstructural protein NCVP2
C;Keywords: nonstructural protein; zinc finger
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A,Status: preliminary
A,Molecule type: DNA
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Typotein - human hepatitis B virus
C;Species: human hepatitis B virus
C;Species: human hepatitis B virus
C;Species: human hepatitis B virus
C;Species: 30-Sep-1993 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C;Accession: A54856
R;Zeng, M.; Huang, B.R.; Cai, L.W.; Pan, G.Z.
Chinese Biochem. J. 12, 22-26, 1996
A;Title: The sequence analysis of the hepatitis B virus (HBV) X gene and its expression i A;Reference number: JC1331
A;Reference number: JC1331 Conserved hypothetical integral membrane protein HP0284 - Helicobacter pylori (strain 266 c) Species: Helicobacter pylori (pate: 09-dug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004 c) Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004 c) R.Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. A.Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N.A.; Rieference number: A64520; MulD:97394467; PMID:9252185 A,Cross-references: UNIPROT:09XV66; EMBL:281512; PIDN:CAB04172.1; GSPDB:GN00023; CESP:F2E C,Genetics: A,Gene: CESP:F25C8.3 A;Map position: 5 A;Introns: 32/2; 57/2; 73/3; 113/3; 157/3; 366/1; 456/1; 509/1; 638/1; 773/2; 848/1; 902/ /3; 2510/2; 2737/3; 2827/1; 2902/3; 3093/3; 3121/1 C;Superfamily: Caenorhabditis elegans hypothetical protein F25C8.3 A;MOlecule type: DNA A;Residues: 1-523 <TOM> A;Cross-references: UNIPROT:025059; GB:AE000547; GB:AE000511; NID:92313377; PIDN:AAD0735; 9 1571 RADKRNILADNWQAKQQALRKSIHARQSTAVPRRESAMVGQPE-FASKAIKMMLMEKMQQ 1629 ų, 54 40 A; Status: preliminary; nucleic acid sequence not shown; translation not shown 55 KKEKVKRSQKATE--FIDYSIEQSHHAILTPLOTHLTMKGSSMKCSSLSSEAILFTLTLQ ----NFPRLPGILA 2 RAFLRN------QKYEDMHNIIHILQIRKLRHRLSNFPRLPGILAPETVLLPFCYKVFR Gaps 32; Gaps DB 2; Length 3147; Indels Length 523; Indels | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 41 PETVL--LPFCYKVFRKKEKVKRSQKATEFIDYSIEQSHHAI 67; 30; atch 11.2%; Score 78; DB 2; cal Similarity 23.5%; Pred. No. 3.9; 24; Conservative 16; Mismatches 30 Query Match
11.3%; Score 78.5; DE
Best Local Similarity 28.1%; Pred. No. 26;
Matches 41; Conservative 17; Mismatches 1683 LVHSPISSVLKCCLL-LSVEQHKQMI 1707 113 LTQ---TLGLECCLLYLSKTIHPQII 135 5 LRNQKYEDMHNIHILQIRKLRHRLS----



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73.5 72.5 72.5 72.5 72.7 72.7 72.7 72.7 72	T 1 1 Q9GZY1	Q9GZY1; 01-MAR-2001 01-MAR-2001 05-JUL-2004 UC28 protein	Name=UC28; Homo sapiens (Human Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9606;	TISSUE Prostate cancer; TISSUE Prostate cancer; MEDLINE 2-1028101; Pubmed=11156405; An G., Ng A.Y., Meka C.S.R., Luo G Wright G.L. Jr., Veltri R.W.; "Cloning and characterization of U prostate, breast, and bladder canc. Cancer Res. 60:7014-7020(2000). EMBL; AF189270; AAG17118.1; EMBL, AR189269; AAG17117.1; Genew; HGNC:21079; PBOV1. SEQUENCE 135 AA; 15722 MW; 2B7]	Query Match Best Local Similarity Matches 135; Conser	1 L	61 RS 	121 CC
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01-AUG-1998 (TrEMBLrel. 07, Created) 01-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Hypothetical protein PH1844. OrderedLocusNames=PH1844;

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RESULT 2 059512 ID 05951 AC 05951 DT 01-AI DT 01-AI DT 01-AI DT 01-AI OF HYPOI GN OTGE:

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                                                                                                                                                        Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DNA Res 5:55-76(1998).
PIR, F71196, F71196
  Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
05-ML-2004 (TrEMBLrel. 27, Last annotation update)
05-ML-2004 (TrEMBLrel. 27, Last annotation update)
Name=F19F19.25 protein (Putative ethylene receptor).
Name=F19F19.25, Synonyms=ERS2;
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Varidiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core endicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Osborne B.I., Vysotskala V.S., Schwartz J.R., Toriumi M., J
Buehler E., Conway A.B., Conway A.R., Dewar K., Feng J., Ki
Kurtz D., Li Y., Shinn P., Sun H., Davis R.W., Ecker J.R.,
Federspiel N.A., Theologis A.,
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
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Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
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Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0009058; P:biosynthesis; IEA.
Complete proteome; Hypothetical protein.
SEQUENCE 381 AA; 42826 MW; EDOEBOCAOCFSCAEI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                       MEDLINE=98344137; PubMed=9679194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 26.8
nes 34; Conservative
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                                                NCBI_TaxID=53953;
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64 KATEFIDYSIEQSHHAILTPLQTHLTMKGSSMKC-SSLSSEAILFTLTLQLTQTLGLECC 122
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 26, Last annotation update)
01-MRA-2004 (TrEMBLrel. 26, Last annotation update)
SI:zK13A21.9 (Novel protein similar to vertebrate microphthalmia-
associated transcription factor (MITF) and zebrafish transcription
factor binding to IGHM enhancer 3a (Tfe3a)).
Name-opnilw2; Synonyms=SI:zK13A21.9;
Name-opnilw2; Synonyms=SI:zK13A21.9;
Buckarydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordatus, Craniatus, Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                        Sakai H., Hua J., Chen Q.G., Chang C., Medrano L.J., Bleecker A.B., Megrowitz E.M.;
Megrowitz E.M.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AC001014; AAB70445.1; ---
EMBL; AF047976; AAC2209.1; ---
PIR; F86174; F86174.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001165; F:two-component sensor molecule activity; IEA.
GO; GO:0001165; P:signal transduction; IEA.
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-!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
EMBL; AL844847; CAE30419.1; -.
INSSP; P25415; JAN4.
Interpro; IPR001092; HLH basic.
Pfam; PP00010; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 645;
                                                                                                                    Hua J., Sakail H., Nourizadeh S., Chen Q.G., Bleecker A.B., Ecker J.R., Meyerowitz E.M.; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46; Indels
Theologis;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
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11.9%; Score 82.5; DE
Best Local Similarity 23.5%; Pred. No. 17;
Matches 31; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR003018; GAF.
Interpro; IPR003061; His kinA N.
Interpro; IPR01052; Prot_amyl_inhib.
Pfam; PF001590; GAF; 1.
Pfam; PF00127; HisKA; 1.
SMART; SM00065; GAF; 1.
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NCBI TaxID=7955,
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Command line parameters:
-MODEL=frame+ n.12p model - DEV=x1h
-MODEL=frame+ n.12p model - DEV=x1h
-MODEL=frame+ n.12p model - DEV=x1h
-DESA_Geneseq_16Dec04 - QFMT=fastan - SUFFIX=n.2p.rag - MINNATCH=0.1 - LOOPCL=0
-DESA_Geneseq_16Dec04 - QFMT=fastan - SUFFIX=n.2p.rag - MINNATCH=0.1 - LOOPCL=0
-LOOPEXT=0 - UNITS=bits - START=1 - RND=1 - MARTEX=blosum62 - TRANS=human40.cdi
-LIST+45 - DOCALIGN=200 - THR_SCORE=pct - THR_MAX=100 - THR_MIN=0 - ALIGN=15
-MODE=LOCAL - OUTFWT=pto - NORM=ext - HEAPSIZE=500 - MINLEN=0 - MAXLEN=200000000
-USRE-SU699974546 @CGN 1 1 2.32 @runat 07092005 174357 19482 - NCFU=6 - ICPU=3
-NO MMAP - LARGEQUERY - NEG_SCORES=0 - WAIT - DSPELOCK=1.00 - LONGLOG
-DEV_TIMEOUT=120 - WARN_TIMEOUT=30 - THREADS=1 - KGAPDP=10 - KGAPEXT=0.5 - FCAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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16226.276 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

    protein search, using frame_plus_n2p model

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geneseqn1980s: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Biomarker Aay59296 Prostate Aay59295 Prostate Aau02174 Biomarker Biomarker Human Human Description Aau02175 | Adr08959 | Aab43292 | Aao06985 | Adq67624 | ADR08959 AAB43292 AAO06985 AAU02174 AAU02175 AAY59296 ü Length DB Query 15.9 15.9 15.9 Score 313.5 308.5 304.5 302 300.5 298.5 694 694 694 Result Š. 10845978

Aae35264 Human P45	378	529	117 Human	Aao08307 Human pol	429 Human	Adm87815 Human EST	Human	Aau76310 Human fas	Adq65903 Novel hum	Aae07113 Human gen	Human	Adg79456 Human sec	Add66320 Novel hum	Human	5 Novel	7 Huma	Aao26240 MDDT rela	Aao06149 Human pol	4 Human	m	54 Human	9 Neural	Adb37543 Neural th	6 Human	NI.	31 Novel	Adb59965 Connectiv	Adm03873 Human pro	Human	Adb37541 Neural th	3 Human	Aau32097 Novel hum	Adr08586 Human pro	Adr09618 Human pro
AAE35264	ABG65578	ADG79629	AAU27917	AA008307	AAM83429	ADM87815	AAE11962	AAU76310	ADQ65903	AAE07113	ADG79555	ADG79456	ADQ66320	AAB94965	ADK37055	ADC86487	AA026240	AA006149	ABB11824	ADE08953	ADS11754	ADB37629	ADB37543	AAG78806	ADK36872	AAU86631	96	ADM03873	AAB95167	ADB37541	ADB65293	0	ADR08586	ADR09618
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ALIGNMENTS

Nucleic acid marker; biomarker; tumour; prostate cancer; bladder cancer; benign prostatic hyperplasia; BPH; breast cancer; human; immunodetection Prostate disease marker UC Band #28 amino acid sequence. Veltri RW Ä AAY59296 standard; peptide; 135 99WO-US013151 98US-00097199 O'hara SM, Ralph D, (first entry) WPI; 2000-116557/10. (UROC-) UROCOR INC N-PSDB; AAZ87584 11-JUN-1999; 12-JUN-1998; WO9964631-A1 19-APR-2000 16-DEC-1999 An G, Homo AAY59296

Novel RNA biomarkers for diagnosis, prognosis and management of prostate, breast and bladder cancer.

Example 5; Page 184-186; 191pp; English

Aao06985 Human pol Adg67624 Novel hum Adk37016 Novel hum Aab92614 Human pro

ADQ67624 ADK37016 AAB92614

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pro

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The inventor. Divoluces include and include to the processor and a fine inventor. Divoluces include the markers are indicators of malignant transformation of prostate, breast and bladder tissues and are diagnostic of the potential of or metastatic spread of malignant prostate tumours. The nucleic acid can also be used as targets for therapeutic intervention in prostate cancer, benign prostatic hyperplasia (BPH), bladder cancer or breast cancer. The markers may be used to design specific probes and primers, for the rapid analysis of prostate, bladder or breast biopsy samples. The probes and primers may also be used for in situ hybridization or in situ PCR detection and diagnosis. They may also be used to identify and isolate full length gene sequences form various BNA libraries. Antibodies against the polypeptide products of the markers can be used to treat prostate cancer, bladder cancer or breast cancer. The encoded proteins may be used to detect antibodies. The proteins and antibodies can be used in immunodetection methods for detecting or quantifying the cancers, and for clinical diagnosis of these cancers. The encoded proteins
                                  invention provides nucleic acid markers of prostate, breast and
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Sequence 135 AA

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158
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           Length:
Matches:
Conservative:
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Prostate disease marker UC Band #28 amino acid sequence
            AAYS9295 standard; peptide; 135 AA
                                                           (first entry)
                                                           19-APR-2000
                                    AAY59295
AAY59295

ID AAYE
XX AC AAYE
XX DT 19-7
XX DE Prof
XX XX DE KW Nuc:
XX XX Nuc:
XX XX HOMK
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Nucleic acid marker; biomarker; tumour; prostate cancer; bladder cancer; benign prostatic hyperplasia; BPH; breast cancer; human; immunodetection

Homo sapiens

218

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338

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398

Diagramments. Division in the markers are indicators of majorate, breast and bladder tissues and are diagnostic of the potential of prostate, breast and bladder tissues and are diagnostic of the potential of or metastatic spread of malignant prostate the mours. The nucleic caid can also be used as targets for therapeutic intervention in prostate cancer, benign prostatic hyperplasia (BPH), bladder cancer or breast cancer. The markers may be used to design specific probes and primers, for the rapid analysis of prostate, bladder or breast bloopsy samples. The probes and primers may also be used for in situ hybridization or in situ PCR detection and diagnosis. They may also be used to identify and isolate the polypeptide products of the markers can be used to treat prostate cancer, bladder cancer or breast cancer. The encoded proteins may be used to detect antibodies. The proteins and antibodies can be used in immunodetection methods for detecting or quantifying the cancers, and for climical diagnosis of these cancers. The antibodies may also be used for radioimaging to quantify and localize the encoded proteins LeuThrProLeuGlnThrHisLeuThrMetLysGlySerSerMetLysCysSerSerLeu 100 399 TCTTCAGAAGCCATATTATTCACATTGACTTTGCAGTTAACTCAGACCCTAGGTCTGGAA 458 RNA biomarkers for diagnosis, prognosis and management of prostate, 61 ArgSerGlnLysAlaThrGluPhelleAspTyrSerIleGluGlnSerHiBHiBAlaIle 41 ProGluThrValLeuLeuProPheCysTyrLysValPheArgLysLysGluLysValLys CTCACACCCTTGCAGACACACTTGACCATGAAAGGTTCCTCAATGAAATGTTCCTCATTA 1 MetargalaPheLeuargasnGlnLysTyrGluaspMetHisAsnIleIleHisIleLeu 21 GinileArgLysLeuArgHisArgLeuSerAsnPheProArgLeuProGlyIleLeuAla 279 AGAAGTCAAAAGGCAACAGAGTTCATTGATTATTCCATAGAACAGTCACACCATGCAATT 159 CAGATCAGAAAATTGAGGCACAGATTAAGTAACTTCCCAAGGCTACCAGGCATTCTAGCT The invention provides nucleic acid markers of prostate, breast 135 0 0 0 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: Example 5; Page 182-183; 191pp; English. US-09-974-546C-85 (1-2506) x AAY59295 (1-135) Veltri RW 99WO-US013151 98US-00097199 'n 694.00 100.00% 100.00% 15.86% breast and bladder cancer. O'hara SM, Ralph WPI; 2000-116557/10. N-PSDB; AAZ87583. (UROC-) UROCOR INC Percent Similarity: Best Local Similarity: Sequence 135 AA; 12-JUN-1998; 11-JUN-1999; 409964631-A1 Alignment Scores: 16-DEC-1999 339 Query Match: Novel An G, ò 셤 셤 원 셤 ò ò ð δ 셤 8

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; TYPE: PRT
; ORGANISM: Human
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    protein search, using frame_plus_n2p model

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Copyright (c) 1993 - 2005
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Sequence 9182, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILLE REPERENCE: CL001307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FEALSEQ for Windows Version 4.0
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114, App
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US-09-663-600A-208

US-09-248-796A-16335

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US-09-248-796A-16335

US-09-248-796A-1144

US-09-663-600A-1144

US-09-663-600A-1144

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US-09-663-111A-121

US-09-652-15-573

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APPLICANT: O'Hara, S. Mark
APPLICANT: O'Hara, S. Mark
APPLICANT: O'Hara, S. Mark
APPLICANT: O'Hara, S. Mark
APPLICANT: O'Hara, S. Mark
TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
TITLE OF INVENTION: PRCGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Nakabilma, Richard A.
REGISTRATION NUMBER: P-42,023
REFERENCE/DOCKET NUMBER: UROC:018
TELECOMMUNICATION INFORMATION:
TELERAN: (512) 474-757
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,787
FILING DATE: 31-UUL-1996
ATTORNEY/AGENT INFORMATION:
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; Sequence 84. Application US/09097199
Patent No. 6218529
; GENERAL INFORMATION:
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APPLICANT: A., Gang
APPLICANT: O'Hara, S. Mark
APPLICANT: Ralph, David
APPLICANT: Veltri, Robert
TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
TITLE OF INVENTION: PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
NUMBER OF SEQUENCES: 9.
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CysCysLeuLeuTyrLeuSerLysThrIleHisProGlnIleIle 135
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MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,199
FILING DATE:
                                                                                                                         Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                  US-09-974-546C-85 (1-2506) x US-09-097-199-84 (1-135)
                                                                                    Length:
Matches:
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/692,787
FILING DATE: 31-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 86, Application US/09097199
Patent No. 6218529
GENERAL INFORMATION:
                                                                                                      694.00
100.00%
100.00%
15.86%
; MOLECULE TYPE: protein US-09-097-199-84
                                                                                                                           Percent Similarity:
Best Local Similarity:
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                                                               Alignment Scores:
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DB:
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Description

Sequence

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TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
                                                                                 0 US-09-974-546-84

0 US-09-974-546-86

0 US-10-121-016-86

1 US-10-121-016-86

5 US-10-122-035-586

5 US-10-123-94-908

1 US-10-123-144-108

1 US-10-123-144-108

5 US-10-203-798-940

5 US-10-203-798-940

5 US-10-198-070-112

4 US-10-198-070-112

4 US-10-198-070-113

6 US-10-198-070-113

6 US-10-108-2604-4121

6 US-10-108-2604-4121

6 US-10-108-2604-4121

7 US-09-00-764-887-145

5 US-10-108-2604-4121

6 US-10-108-2604-4121

7 US-09-800-729-193

8 US-10-108-282-193

1 US-09-800-729-193

1 US-09-980-993-993-952-165

1 US-09-981-982-993-918-165

1 US-09-981-982-993-918-165

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Publication No. US2030050470A1
GENERAL INFORMATION:
APPLICANT: An, Gang
O'Hara, & Mark
Ralph, David
Veltri, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: P.O. Box 4433 CITY: Houston
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CORRESPONDENCE ADDRESS:
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                                Length
                                                                                           COUNTRY: USA
ZIP: 77210
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-Q=/Cgn2 1/USPTO spool/US09974546/runat 07092005_174400_19612/app_query.fasta_1.4942
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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -STARR=1 - END=-1 - MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct - THR MAX=10
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-NORUGE - ICPU=3 -NO MMAP -LARGEQUERY - NEG GCORE=0 -WAIT - DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 - THRRANDS=1 -XGAPPOF=10 -XGAPEXT=0.5
-FGAPOP=6 - FGAPEXT=7 -YGAPOP=10 - YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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13965.459 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                 - protein search, using frame_plus_n2p model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Database :

Sequence 2, Appli Sequence 1659, Ap Sequence 352, App

Sequence

Sequence Sequence Sequence

COMPUTER READABLE FORM:

SUMMARIES

Sequence 201, App Sequence 940, App Sequence 940, App Sequence 1108, App Sequence 112, App Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 31, Appl Sequence 145, Appl Sequence 1763, Appl Sequence 1763, Appl Sequence 1913, Appl Sequence 1913, Appl Sequence 1913, Appl Sequence 1913, Appl Sequence 282, Appl Sequence 282, Appl Sequence 282, Appl Sequence 282, Appl Sequence 282, Appl Sequence 282, Appl Sequence 282, Appl Sequence 282, Appl Sequence 282, Appl Sequence 282, Appl Sequence 282, Appl Sequence 282, Appl Sequence 282, Appl Sequence 283, Appl Sequence 283, Appl Sequence 283, Appl Sequence 283, Appl Sequence 284, Appl Sequence 283, Appl Sequence 283, Appl Sequence 283, Appl Sequence 283, Appl Sequence 233, Ap

Total number of

Searched:

score:

Title: Perfect

Sequence:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/974,546
FILING DATE: 10-Oct-2001
CLASSIFICATION: Unknown
PRIOR APPLICATION NUMBER: 09/097,199
PILING DATE: 1998-06-12
ATTORNEY/AGENT INFORMATION:
NAME: NAKABHIMA, RIChard A.
REGISTRATION NUMBER: P-42,023
REFERENCE/DOCKET NUMBER: UROC:018
TELECAMUNICATION INPORMATION:
TELECAMUNE (512) 418-3000
TELECAMUNE (512) 474-7577
INFORMATION POR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acids
TYPE: amino acids
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 84:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 86, Application US/09974546
Publication No. US20030050470A1
GENERAL INFORMATION:
APPLICANT: An, Gang
O'Hara, S. Mark
Ralph, David
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100.00%
100.00%
15.86%
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Best Local Similarity:
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Velti, Robert
TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
                                                                                                                                                                                                                                                                                                                      COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/974,546
FILING DATE: 10-0ct-2001
CLASSIFCATION: Unknown
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/097,199
FILING DATE: 1998-06-12
ATTORNEY/AGENT INPORMATION:
NAME: Nakeshima, Richard A.
REGISTRATION NUMBER: P-42,023
REFERENCE/DOCKET NUMBER: UNCC.018
TELECOMMUNICATION INPORMATION:
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Matches:
Conservative:
Mismatches:
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                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
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thromboxane A-2 re

transforming prote

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Run on:

Sequence:

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C;Comment: This "warning" entry is a conceptual translation in all 6 reading frames of or in-frame stop codons are shown as 'X'.
C;Comment: Any significant similarity of a predicted protein sequence to a portion of thi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics 12, 838-841, 1992
A;Title: Identifying coding exons by similarity search: Alu-derived and other potentiall)
A;Reference number: A40200; MUID:92241891; PMID:1572661
A;Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
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Matches:
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JC5238
A47582
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I78885
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A56194
T02670
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B71619
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A;Reference number: A40201
A;Accession: C40201
A;Molecule type: DNA
A;Residues: 1-613 <CLA>
R;Clayerie, J.M.
                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
           C, Accession: C40201
R, Claverie, J.M.
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Pred. No.:
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-MODEL=frame+ n2p.model -DEV=xlh
-Q=/CGD2 1/USFTO spool/10809974546 frunat 07092005 174358 19508/app query.fasta_1.4942
-Q=/CGD2 1/USFTO spool/10809974546 frunat 07092005 174358 19508/app query.fasta_1.4942
-DB=PIR 79 -QFWT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=Dits -START=1 -ENN=-1 -MATRIX=blooum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-UNITS=DITS -NORM=EXT -HEAPSIZE=500 -MINLEN=0 -MAXIEN=2000000000
-USER=US09974546 @CGN 1 1.79 @runat .D19BLOCK=100 -LONGLOG -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7
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Copyright (c) 1993 - 2005 Compugen Ltd
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Fgapop 6.0 , Fgapext
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A; Molecule type: DNA
A; Residues: 1-597 < CLA>
R; Claverie, J.M.
Genomics 12, 838-841, 1992
A; Title: Identifying coding exons by similarity search: Alu-derived and other potentially
A; Reference number: A40200; MUID: 92241891; PMID: 1572661
A; Contents: annotation
C; Comments: This "warning" entry is a conceptual translation in all 6 reading frames of or in-frame stop codons are shown as 'X'.
C; Comment: Any significant similarity of a predicted protein sequence to a portion of thi
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A;Reference number: A40201
A;Accession: B40201
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A;Accession: E40201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2227 GGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGA-----GGTGGGTGGATCACC 2280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2341 ACACAAAAATTAGCCGGGCGTGGTGGCACATGCCTGTAATCCCAGCTACTCAGGAGGCT 2400
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C;Species: Homo sapiens (man)
C;bacies: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
C;Accession: E40201
R;Claverie, J.M.
                                                 ::||)
227 etargProGlyValargAspGlnProGlyGlnHisGlyLysThrProPhe-LeuLeuLys
                                                                                                                                                             2304 GCTGGTCTCGAACTCCCGACCTCAGGTGATCCACCCA-----CCTCCCAAAGTGCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2281 TGAGGTCGGGAGTTCGAGACCAGCCTGACCAGCATGGTGGAACCCCCATCTTACTAAAA
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A,Molecule type: DNA
A,Residues: 1-597 <CLA>
K.Claveridues: 1-597 <CLA>
K.Claveridues: 1.597 <CLA>
A,Title: Identifying coding exons by similarity search: Alu-derived and other potentiall)
A,Reference number: A40200; MUID:92241891; PMID:1572661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Contents: annotation
C; Comment: This "warning" entry is a conceptual translation in all 6 reading frames of or
in-frame stop codons are shown as 'X'.
C; Comment: Any significant similarity of a predicted protein sequence to a portion of thi
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C;Species: Homo sapiens (man)
C;Dacte: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000
C;Accession: E40201
R;Claverie, J.M.
                                                                                                                                                                                                2495 AGTTTTACTCCTGTTGCCCAGGCTGGAGTGCAATAGTGCAATCTCAGCTCACC----GCA
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MEDLINE=21028101; PubMed=11156405;
An G., Ng A.T., Meka C.S.R., Luo G., Bright S.P., Cazares L.,
Wright G.L. Jr., Veltri R.W.;
"Cloning and characterization of UROC28, a novel gene overexpressed in
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Catarrhini, Hominidae, Homo.
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Cancer Res. 60:7014-7020(2000).
EMBL, AF189269; AAG17118.1; -.
Genew, HGNC:21079; PBOV1.
SEQUENCE 135 AA; 15722 MW; 2B7DB8B198
                                            Q9NX17
ALU8 HUMAN
Q6ZSZ8
ALU8 HUMAN
Q6ZNZ7
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Q8N7M7
Q6ZSG8
Q96NR6
Q6ZTX8
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Q6ZSN3
Q8N2A0
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Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
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01-MAR-2001 (TrEMBLrel. 16,
05-UUL-2004 (TrEMBLrel. 27,
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                          - protein search, using frame_plus_n2p model
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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1: uniprot_sprot:*
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and is derived by analysis of
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J. Mol. Evol. 27:194-202(1988).
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                                                                                                                                                                                                                                                                   41 ProGluThrValLeuLeuProPheCysTyrLysValPheArgLysLysGluLysValLys
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"Identifying coding exons by similarity search: alu-derived and other
potentially misleading protein sequences.";
Genomics 12:838-841(1992).
   CAGATCAGAAAATTGAGGCACAGATTAAGTAACTTCCCAAGGCTACCAGGCATTCTAGCT
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-FEB-1995 (Rel. 31, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Alu subfamily SP sequence contamination warning entry.
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J. Mol. Evol. 32:105-121(1991).
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MEDLINE=91178815; PubMed=1706781;
Jurka J., Milosavljevic A.;
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Nature 371:752-752(1994)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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             primate genomes with an average spacing of 4 kb. Some of them are actively transcribed by pol III. Normal transcribes may contain Alu-derively transcribed by pol III. Normal transcribes may contain can derively transcribes and contain by a light of the sequence of a variate and/or rearranged cDNAs lighted with Alu-derived sequence in any orientation. Although Alu elements (especially situated on the complementary strand) have a great potential to create additional/alternative exons, consideration should be given to the possibility that the presence of an Alu in an open reading frame may have resulted from a cloning artifact or may be due to misinterpretation of sequencing data. This point has been overlooked on several occasions, with
                                                                                                                                                                                                                 the consequence of erroneous Alu-derived amino acid sequences being reported.

CAUTION: Any significant similarity of a putative protein sequence with an Alu-translated entry must be taken as a warning that a part of Alu repeat may have been artifactually included in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 SerProGluValGlySerSerArgProAla***ProThrTrpArgAsn-ProValSerTh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 rLysAsnThr-LysIleSerArgAlaTrpTrpArgMetProVallleProAlaThrArgG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2222 GGCCAGGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGG-----GAGGTGGGTGGA
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CAUTION: Alu repetitive sequences are interspersed in human and
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Conservative:
Mismatches:
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Frame-3.
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ProDom, PD003738; GIDA; 1.
Hypothetical protein.
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1 (bases 1 to 2512)
An,G., Mg,A.Y., Meka,C.S., Luo,G., Bright,S.P., Cazares,L., Wright,G.L. Jr. and Veltri,R.W.
Cloning and characterization of UROC28, a novel gene overexpressed cancer Res. 60 (24), 7014-7020 (2000)
AC010598 Homo sapi
AC104588 Homo sapi
AC104582 Homo sapi
AC034102 Homo sapi
AC034102 Homo sapi
AC034264 Homo sapi
AC032615 Homo sapi
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AL13696 Human DNA
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Homo sapiens UC28 protein (UC28) mRNA, complete cds.
AFIB9269
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/tissue type="prostate cancer"
1. .2512
/gene="UC28"
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An,G. and Veltri,R.W.
Direct Submission
Submitted (23-SEP-1999) UroSciences, U
Parkway, Oklahoma City, OK 73104, USA
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AC069004
AC137723
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Copyright (c) 1993 - 2005 Compugen Ltd.
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100.0%; Score 2505.6; DB 9; Length 2512; Conservative 0; Mismatches 0; Indels 0; Gaps GACCTTAAAITATACGAGGGCAATTCAGTGTATAATTACAAAITATTCTTCTA GACCTTAAAITATACGAGGGCAATTCAGTGTATAATTACAAATTATTCTTCTA GACCTTAAAITATACGAGGGCAATTCAGTTAAATTTACAAAATTATTCTTCTA GACCTTAAAAITATACGAGGGCAATTCAGTGAGGCCCCCTGAGGGCCTTCTTAAGGACC TTGCTACAGAGTTACAATTTACAGTTAAGTAAATTTACAAAATTATTTACAAATTCTTCTAAGGAACC AGAAATTGGGGATATCCAATTATACACTACAATTTACAGAAATTGGGCACA GAAAATTGGGGATATCCAATTATATCCAATTTACAGAAATTGAGGCACA GAAAATTGGGGATATCCAATTATATCCAATTTACAGATCAGAAAATTGAGGCACA GAAAATTGGGGATATCCAATAATATATCCAATTTACAGATCAGAAAATTGAGGCACA GAATTAGGGATATTCCAAGGCAATATTATTACAATTCAGAAATTGAGGCACA GAATTAGGATATTCCAAGGCAATATTATTACAATTCAGAAATTGAGGCACA GAATTAGGATATTCCAAGGCAATATTATTACAATTCAGAAAATTGAGGCACA GAATTAGGATATTCCAAGGCAATATTATTACAAATTCAGAAAATTGAGGCACAAGAT TCAGTGATTATTCCAAAGGATACTCAAGCAATTCTCACAAAAATTGAGGCACAAGAT TCAGTGATTATTCCAAAGGCAATATTACAAAATTGAGAACACATTTACAAAATTGAGGCACAACACT TCATTGATTATTCCAAAAAAAAAA
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone amen. Note that the variation annotation may not be found in the sequence submission only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) = 30); an attempt was made to resolve all sequencing problems, such one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information or the WORMPEP database can be found at the primary accession thromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at the their source databases:

RPI-17111 is from the library RPCI-1 constructed by the group of price and a found at the condition of the condition of the feature described by the Sanger centre Chromosome form por further and preserved by the group of
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2400 GAGGCGGAGAATTGCTTGAACCCGGAAGGTGGAGGTTGTTGCGGTGAGCTGAGATTGCAC 2459
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (04-MAR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On May 13, 1999 this sequence version replaced gi:4582115.
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Human DNA sequence from clone RP1-171N11 on chromosome 6q23,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Pred. No. 0;
1; Mismatches
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Contact: humquery@sanger.ac.uk
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1 GACCTTAAATATCGAGGTGGCTAATTGATGATAATTACAAAATTATTCTTCTA 60 29796 GACCTTAAATATATCGAGGTGGCTAATTGATGATAATTTACAAAATTATTCTTCTA 29855 61 TTGCTACAGAGCTGACTAATTACAGTGGCCACCATGAGGCCTTCTTAAGGAACC 120 29856 TTGCTACAGAGCTAATTTACAGTAGCCACCATGAGGGCCTTCTTAAGGAACC 29913 121 AGAAATTGAGAGCTACAATTTACAGTATTACAGTTTACAGACACTAGGGAACC 29913 121 AGAAATTGAGGATATGCACAATTTATTCACATTTACAGATCAGAAATTGAGGCACA 180 29914 AGAAATATGAGGATATGCACAATATTATCACATTTACAGATCAGAAAATTGAGGCACA 29973 181 GATTAAGTAAGTAACTTCCCAAGGCATTCTAAGAATTGAGGCACA 29973		TGACCATGAAAGGTTCCTCAATGAAATGTTCCTCATTATCTTCAGAAGCCATATTATTCA	AAACTATACATCCACAGATCATATAAACTCTCAGCCCTGCTGCAAAGCCTTTCCAGAAA AAACTATACATCCACAGATCATAAAACTCTCAGCCCTGCTGCAAAGCCTTTCCAGAAA AAAAAAATGGTTGAAAAGCAATTCTGCTACCCATGATGAAAGCCCTTTCCAGGAAA ATAAAAATGGTTGAAAAGGCAATTCTGCTACCCAATGACTGTTAAGCCCAGCCAAGTAAC	TGAACCATTCCAACTTACTTATGAAAAGAATTTGATGATGATGGCCCCCCCC	ATTATCTCAATTTAGTTTGTTATTTATCCTAGTGGGCCATTAAAAACTACCACATGTGTT 7	30574 TCTGTCTCCGGTTAGTCAATAACTAAACGAGGAATTAGTAAGCCATGTGCCAGAT 30633 841 GCTCCGCTAGGCACCAGGGATAAAAACAATACTTATAGTATACCACTAATTTCGCTT 900 30634 GCTCCGCTAGGCACCAGAGGGATAAAAACAATACTTATAGTATACCACTAATTTCGCTT 30693 901 AGTAACTAGTGAAATGTTCAAGTCATGCCTGAGTCAAGAGTTACAGAGAGAG	30694 AGTAACTAGTGAAATGTTCAAGTCATGCCTGAGTCAAGAGTTGAGAGACATTACAATGT 30753 961 GTAATGGAAACCAAGGAAACTTTGGATAAGTGGGACTTAGTGTTTATATATA	1021 TAATHGATHTCTGACTCTATCACTTGGCCTCCAAACACAGATHGTGTTTHCTHTGGTTTT 1080

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Best Local Similarity 99.5'
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Waterston, R.H.
Direct Submission
Submitsed (Or.APR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Sep 1, 2000 this sequence version replaced gi:7523932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 186698)
Waterston, R. H.

The sequence of Homo sapiens clone
Unpublished
                                                                                                                                                           2340 AACACAAAAATTAGCCGGGCGTGGTGGCACATGCCTGTAATCCCAGCTACTCAGGAGGC
                                                                                                                                                                                                                     TGAGGCGGAGAATTGCTTGAACCCGGAAGGTGGAGGTTGTTGCGGTGAGCTGAGATTGCA
                                                                                                    CTGAGGTCGGGAGTTCGAGACCAGCCTGACCAGCATGGTGGAACCCCCATCTCTACTAAA
                                            CCGGCCAGGCACGGTGCTCACGCCTGTAATCCCAGCACTTTGGGAGGTGGGTCGATCAC
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                                                                                                                                                                                                                                                                                              32249 CTATTGCACTCCAGCCTGGGCAACAGGAGTAAAACTCCCCCCCACCC 32295
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Center code: WUGSC
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AC036236.2 GI:9958166
HTG; HTGS_PHASE1; HTGS_DRAFT.
HOMO sapiens (human)
                                                                                                   2280
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VERSION
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SOURCE
ORGANISM
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DEFINITION
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159156 GACCTTAAATATATGGAGGGGGGGTAATTGATGTATAATAATTACAAAATTATTGTTCTTCTA 159215
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This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                             4769: contig of 4769 bp in length
4869: gap of unknown length
11677: contig of 6788 bp in length
11578: gap of unknown length
1158 28189: contig of 16432 bp in length
1190 28289: gap of unknown length
1190 53341: contig of 25622 bp in length
1242 53441: gap of unknown length
1242 102377: contig of 48886 bp in length
1242 102377: contig of 48886 bp in length
1242 102427: gap of unknown length
1242 182881: gap of unknown length
1282 182881: gap of unknown length
1282 182881: gap of unknown length
1282 18698: contig of 80354 bp in length
1292 186698: contig of 3817 bp in length
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/note="assembly_name:Contig10"
4870. 11657
/note="assembly_name:Contig11"
11758. 28189
/note="assembly_name:Contig12"
28290. 53341
/note="assembly_name:Contig13"
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99.5%; Pred. No. 0;
tive 1; Mismatches
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/db_xref="taxon:9606"
/chromosome="6"
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	160834 CCTCCAACAACGACATTCAGGAGTTAAATATTTTTCATCAACATTGGTTTTTCCTT 160893 1740 AACGCTAGAGATTGCTACAAATCTTCTGAAGGTCTCAATGGCTTCAGGCTAAGAAGAG 1799 160894 AACGCTAGAGATTGCTACAAATCTTCTGAAGGGTCTCAATGGCTTCAGGCTAAGAAGAG 160953 1800 TTTCTCCCTGTTATAAGCAACAAATTAGCCATTTCACTCTCAAAGAGA 160953 160954 TTTCTCCCTGTTATAAGCAAAAATTAGCCATTTCACTCTCAAATG 1859 1860 ATTCTCCCTGTTATAAGCAAAAAATTAGCCATTTCACTCTCAAAATG 161013		GACAGTACTGATACATAATTTAAAAGCACACTCCCTTCCACTTTGGTAATACCAGAACTC [2160 ATTCACTCATCTGTATTTCTATAGATGTTTACTAGGGGTTTGTTATAAAATAC 2219	161432 CTGAGGTCGGGGTTCGAGACTGCCTGACCAGCATGGTGGAACCCCCATCTCTACTAAA 161491 2340 AACACAAAAAATTAGCCGGGCGTGGTGGCACTGCTGAATCCCAGCTCTCTCT	
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Qy 421 CATTGACTTTGCAGTTAACTCAGACCCTAGGTCTGGAATGCTGTTCTTCTTCTTACTTA		OY 781 TCTGTCTCTCCATTAGTCAATAACTAAACGAGCAATTAGTAAGCCATGTGCCAGAT 840	Db 160054 AGTAACTAGAAATGTTCAAGTCAAGACTAAGAGTTGAGAGAGA	GTTTTCTTCACTATGGGATCTTCTGTGCCCAGCACAGTGCCTGACACATAGAAACAATC	160354 TAGAACATCCAGAGTAAGTGATGAGGCCTCTGCATTTATATGCGCTTAAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAAAATTAAGAAAAATTAAGAAAAATTAAGAAAAAA	Qy 1380 GCATAAACTATTAAAGGAAAATCACATCTCCAGGCTTTCAATGTTTGTT

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                                             122 GAAATATGAGGATATGCACAATATTATTCACATTTTACAGATCAGAAATTGAGGCACAG
                                                                                  119 GAAATATGAGGATATGCACAATATTATTCACATTTTACAGAAAATTGAGGCACAG
                                                                                                                                    182 ATTAAGTAACTTCCCAAGGCTACCAGGCATTCTAGCTCCAGAAACTGTGCTCTTACCATT
                                                                                                                                                                ATTAAGTAACTTCCCAAGGCTACCAGGCATTCTAGCTCCAGAAACTGTGCTCTTACCATT
                                                                                                                                                                                                                       CTGCTACAAGGTATTTCGAAAAAAAGAAAAAGTAAAAAGAAAAGGAACAAAGGCAACAGAGTT
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                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

12. (basea 1 to 2456)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Colling, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhar, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Earmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, W.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Rahs, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Sanilus, D.E.,
Schnerch, A., Schein, J. B., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

1277732 1.2022)
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Location/Qualifiers
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Submitted (16-APR-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ACCTIAAATATATCGAGGTGGCTAATTGATGTATAATAATTTACAAAATTATTCTTCTAT
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Contact: MGC help desk
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: Anup Madan, University of Iowa
CDNA Library Preparation: Anup Madan, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Neurogenomics Research Lab,
200 B EMRB, University of Iowa, Iowa City, IA-52242
anup-madan@uiowa.edu
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mol_type="mRNN"
db xref="taxon:966"
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                      GI:46575743
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Best Local Similarity 99.4<sup>1</sup>
Matches 2488; Conservative
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BC069109.1
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                                          ACACAAAAATTTAGCCGGGCGTGGTGGCACATGCCTGTAATCCCCAGCTACTCAGGAGGCT
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An,G. and Veltri,R.W.
Direct SUbmission
Submitted (23-SEP-1999) UroSciences, U
Parkway, Oklahoma City, OK 73104, USA
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/organism="Homo sapiens"
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2047. .2052
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                                                              TGGTGGTGCTTTAAAAAGATATTAATAGATAATATGAAAAATCTCCCATCTCAAAAATAATG
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/protein_id="AAG17118.1"
/db_xref="G1:1041604"
/translation="WRAFLENGKYEDMENTHILDIRKLRHRLSNFPRLPGILAPETV
LLEPCYKVFRKKEKVKRSQKATEFIDYSIEGSHHAILTPLQTHLTMKGSSMKCSSLSS
ELFTLTLQLTQTLGTEGCLLYLSKTIHPQII"
1961. 2103
/gene="UC28"
2453
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Bukaryota, Matazoa; Chordata, Craniata, Vertebrata; Buteleostomi;
Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 2103)
An,G., Ng,A.Y., Maka,C.S., Luo,G., Bright,S.P., Cazares,L.,
Mright,G.L. Jr. and Veltri,R.W.
Cloning and characterization of UROC28, a novel gene overexpressed
in prostate, breast, and bladder cancers
Cancer Res. 60 (24), 7014-7020 (2000)
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Homo sapiens UC28 protein (UC28) mRNA, complete cds.
AF189270
                                            TATTGCACTCCAGCCTGGGCAACAGGAGTAAAACTCCCCCCCA 2503
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/gene="UC28"
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Score 1950, DB 6; Length 2087, Pred. No. 0; 0; Mismatches 10; Indels 1; Gaps 3TGGCTAATTGATGATAATAATTTAACAAATTATTCTTCA GTAATTTACAGTAGGCCCCATGAGGGCCTTCTTAAGGAACC 1CAATTTACAGTAGGCCCCATGAGGGCCTTCTTAAGGAACC 1CAATTTACAGTAGGCCCATGAGGGCCTTCTTAAGGAACC 1CAATTTACAGTAGGCCCATGAGGGCCTTCTTAAGGAACC 1CAATTTACAGTAGGCCCATGAGGGCCTTCTTAAGGAACC 1CAATTTACAGTAGGCCCATGAGGGCCTTCTTAAGGAACC 1CAATTTACAGTAGGCCCATGAGGGCCTTCTTAAGGAACC 1AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	ò a	රු යි	දුර දුර	ç d	දු පු	රු දි	S S	ර් සි	ර් සි	ò q	상 음	& A	දු පු	P &	දුරු අධ	දු පු	\$ g	RESULT AR14675 LOCUS
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	ocation/Qualifiers 2087 organism="unknown" mol_type="unassigned DNA	Score 1950; DB 6; Length 2087; Pred. No. 0; 0; Mismatches 10; Indels 1; Gaps				ACCAT	AGAGT			ATCCA 				rater 	STGTT	CAGAT		

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Submitted (30-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 137227)
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Direct Submission
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                                                                                                                        1 (bases 1 to 757)
An,G., O'Hara,S.Mark., Ralph,D. and Veltri,R.
Biomarkers and targets for diagnosis, prognosis and management prostate, breast and bladder cancer
Prostate, breast and 3 17-AAR-2001;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                        DB 6; Length 757;
                                                                                                                                                                                                                                                                                                                     Query Match 25.0%; Score 626.2; DB 6; Length 7 Best Local Similarity 94.6%; Pred. No. 1.6e-123; Matches 716; Conservative 0; Mismatches 28; Indels
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                                                                                                                                                                                                                                                                  /mol_type="unassigned DNA'
Sequence 3 from patent US 6218529.
AR146757
AR146757.1 GI:15109946
                                                                                                                                                                                                                                 1. .757
/organism="unknown"
                                                                                                        Unclassified
                                                                     Unknown
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COMMENT

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166895 bp DNA linear HTG 08-APR-2000
Homo sapiens chromosome 3 clone RP11-200119 map 3, WORKING DRAFT
AC023415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/note="overlaps bases 1. .2004 of clone AC023797"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.0%; Score 201.6; DB 9;
Best Local Similarity 85.3%; Pred. No. 5.1e-33;
Matches 249; Conservative 0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /standard_name="SHGC-77693"
99577. 99720
/standard_name="RH102770"
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17480. .97732
                                                           standard name="SHGC-77695"
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95496. .9<u>5</u>654
                                                                                                                                                                                                                                                                                                                                                         /standard_name="WI-22352"
            _name="SGC38304'
                                                                                          ard_name="RH99296"
.94510
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94393. .94560
                                                                                                                                                                                                                                                         /standard_name="RH66305"
95498. .95656
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Homo sapiens chromosome 3, clone
Unpublished
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
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AC023415
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                                                                                                                                                                                                                                                                                                                    CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at URL:
http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht
                                                                                                             Direct Submission
Submitted (26-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Molecular and Human Genetics, Baylor Diaza, Houston, TX 77030, USA
On Sep 3, 2002 this sequence version replaced gi:22549647.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
Submitted (03-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 137227)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="Polymorphism between Baylor BACS (C/T)."
function="polymorphic site"
40291. .40674
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12419. .42420
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/db_xref="taxon:9606"
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.63697
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/clone="RP11-200119"
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                                                                                        Worley, K.C.
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                                                                                                AUTHORS
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2326

Gaps

4

Indels

Length 137227;

4436

and Lander, E. RP11-200119

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100 bp
1 of 5136 bp in length
1 100 bp
3 of 4237 bp in length
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of 4589 bp in length
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of 5684 bp in length
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of 3185 bp in length
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of 5086 bp in length
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note="assembly_fragment"
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8926. .22110
note="assembly_fragment"
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note="assembly_fragment"
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note="assembly_fragment"
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/note="assembly_fragment"
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note="assembly_fragment"
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35559, .40046
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/mol_type="genomic DNA"
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/chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Chongellano, K., Colangellano, K., Colangellano, K., Colangellano, K., Dodge, S., Domino, M., Doyle, M., Perestor, J., Ferreira, P., FitzHugh, M., Forrest, C., Gage, D., Galdgan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heafcord, A., Horton, L., Klein, J., Landers, T., Largocque, K., Lehcozky, J., Lernhe, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarth, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Miranda, C., Menanga, V., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Peterson, K., Plerre, N., Pisani, C., Pollara, V., Raymond, C., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wux, Myman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and
                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center clone name: 200_119
Sequencing vector: M13, M77815, 10% of reads
Sequencing vector: M13, M77815, 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 16794 bases at least Q40
Consensus quality: 160262 bases at least Q30
Consensus quality: 162545 bases at least Q20
Insert size: 171000; agarose-fp
Insert size: 164295; aum-of-contigs
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
Quality coverage: 4.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L6745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1021: contig of 1021 bp in length
1121: gap of 100 bp
2188 contig of 1067 bp in length
2188: gap of 100 bp
3869: contig of 1581 bp in length
3969: gap of 100 bp
5120: contig of 1051 bp in length
5120: gap of 100 bp
6753: contig of 1051 bp in length
6833: gap of 100 bp
8166: contig of 1313 bp in length
8266: gap of 100 bp
961: contig of 1319 bp in length
9761: gap of 100 bp
9761: gap of 100 bp
12386: contig of 2625 bp in length
12486: gap of 100 bp
12586: gap of 100 bp
12586: gap of 100 bp
15588: gap of 100 bp
15588: gap of 100 bp
15588: gap of 100 bp
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12487
15619
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COMMENT

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Consensus quality: 163237 bases at least 040
Consensus quality: 165500 bases at least 030
Consensus quality: 166457 bases at least 030
Consensus quality: 166457 bases at least 030
Estimated insert size: 170000; agarose-fp estimation
Estimated insert size: 170161; sum-of-contigs estimation
Quality coverage: 14.19 in 020 bases; agarose-fp estimation
Quality coverage: 14.39 in 020 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2387 CTACTCAGGAGGCTGAGGC-GGAGAATTGCTTGAACCCGGAAGGTGGAGGTTGTTGCGGT 2445
                                        Submitted (20-FEB-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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85.3%; Pred. No. 5e-33;
tive 0; Mismatches 39; Indels 4;
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gap of unknown length
contig of 92206 bp in length
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of 1265 bp in length
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of 1124 bp in length
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/clone_lib="RPCI human BAC library 11"
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unknown len
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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/chromosome="16"
                                                                                                                                         Web site: http://www.jgi.doe.gov
                                                                                                                                                                                               Center Project Name: 408775
Center clone name: RPCI-11_6E10
                                                                                -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
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      DOE Joint Genome Institute.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105261 GCAGGTGGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTAAAACCCC 105320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105321 CGTCTCTACTAAATTACAAAATTAGCTGGGCGTGGTGGGACATGCCTGTAATCCCAG 105380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 17096).

DOB Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATCTCTACTAAAAACACAAAAATTAGCCGGGCGTGGCGACATGCCTGGTAATCCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2446 GAGCTGAGATTGCACTCCAGCCTGGGCAACAGGAGTAAAACTCC 2497
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HTG; HTGS PRASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.0%; Score 201.6; DB 2;
Best Local Similarity 85.3%; Pred. No. 5e-33;
Matches 249; Conservative 0; Mismatches 39;
                                                                                                                                                                                                         63103. 70861 - 70862 / 70962 - 76669 / 7000 - 8888mbly_fragment" / 70962 / 76669 / 7000 - 8888mbly_fragment"
                                                                                                                                                                     57917. .63002
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84204. .91221
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127063. .166895
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101055. .109879
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2 (bases 1 to 170961)
                                                                      note="assembly_fragment
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AC112202
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Web site: http://www.hgsc.bcm.tmc.edu/
Draftling Center Code: BCM
Contact: hgsc.help@bcm.tmc.edu
Center project Information
Center project name: HBKP
                                                                                                      Center: Baylor College of Medicine
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1. 174054
/ organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="RP11-6223"
                                                                                                                                                                                                                                                                                        Center clone name: RP11-622J3
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MAMMALIA BULKDATIA Primates Catarrhini, Hominidae, Homo.

1 (Dases I to 17462)

2 (Dases I to 17462)

2 (Dases I to 17462)

3 MAIRY, D. M., Adams C., Adio-Oduola B., Ali-Osman, F.R., Allan, C., Adio-Oduola B., Ali-Osman, F.R., Allan, C., Adams C., Adio-Oduola B., Ali-Osman, F.R., Banks T., Barbaria, J., Bench, B., Burkel, T., Barbaria, J., Bench, B., Burkel, T., Barbaria, J., Bench, P., Burkel, T., Barbaria, J., Bench, P., Burkel, R., Bimage, K., Blanck, J. Brayal, M. Baryati, N.P., Buhay, C., Burch, P., Burkel, C., Burrell, K.L., Byrd, N.C., Carrer, M., Carter, M., Cavazoa, S.R., Chacko, J., Chavez, D., Chen, Z., Chodhyy I., Christopoulos, C., Clava's, C., Davy, Carroll, L., Dederich, J. Onth, H. H., Douthwaite, K.J., Draper, H., Dugan, Rocha, S., Dutbin, K., Delaney, K.R., Delack, C., Davy, Carroll, L., Dederich, B., David, R., Douthwaite, K.J., Draper, H., Dugan, Rocha, S., Dutbin, K.J., Barnhart, C., Edgar, D., Edwards, C.C., Barrell, C., Escotto, M., Falls, T., Perraguco, D., Padgy, C., Pord, J., Roster, P., Francis, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Lud, M., Marris, C., Lud, M., Marris, C., Lud, C., Lud, M., Marris, C., Lud, M., Marris, C., Marris, C., Marris, C., Marris, C., Marris, C., Marris, C., Marris, C., Marris, C., Marris, C., Marris, C., Marris, C., Marris, C., Marris, C., Marris, C., Marris, C., Marris, C., Marris, C., Marris, C., Marris, C.
93501 CTACTCAGGAGGCTGAGGCAGGAGAATTGCTTGAACCCGGGAGGTGGAG---GCTGCAGT 93557
                                                                                                                                                                                                                                                                DNA linear HTG 21-SEP-2002
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                                                                                                            93558 TACCTGAGATTGCCCCATTGTACTCCAGCCTGGGCAACAAGAGCGAAACTCC 93609
                                                                              2446 GAGCTGAGATTGCACTATTGCACTCCAGCCTGGGCAACAGGAGTAAAACTCC 2497
                                                                                                                                                                                                                                                             AC131148
Homo mapiens clone RP11-622J3, *
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Homo sapiens (human)
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KEYWORDS
SOURCE
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2326 NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Sep 21, 2002 this sequence version replaced gi:22296651. 14631 AAATAGCAAATGGAAGGCTGGGCACGGTGGCTCACACCTGTAATCCTGGCACTTTGGAAG 2327 CATCTCTACTAAAAACACAAAAAATTAGCCGGGCGTGGTGGTGGCACATGCCTGTAATCCCAG 14511 CGTCTCTACTAAAATTACAAAAATTAGCTGGGGCGTGGTGGGGACATGCCTGTAAATCCCAG 2387 CTACTCAGGAGGCTGAGGC-GGAGAATTGCTTGAACCCGGAAGGTGGAGGTTGTTGCGGT 2207 ATATAAAAATACCCCGGCCAGGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAG 2267 GTGGGTGGATCACCTGAGGTCGGGAGTTCGAGACCAGCCTGACCAGCATGGTGGAACCCC 14451 CTACTCAGGAGGCTGAGGCAGGAGAATTGCTTGAACCCGGGAGGTGGAG---GCTGCAGT 4; Gaps 2446 GAGCTGAGATTGCACTATTGCACTCCAGCCTGGGCAACAGGAGTAAAACTCC 2497 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. 8.0%; Score 201.6; DB 2; Length 174054; 85.3%; Pred. No. 5e-33; tive 0; Mismatches 39; Indels 4; 0 Sequencially vectors: Plasmid;
Sequencially vectors: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 170243 bases at least Q40
Consensus quality: 170621 bases at least Q20
Consensus quality: 170621 bases at least Q20 9948: gap of unknown length 30170: contig of 2022 bp in length 30270: gap of unknown length 51230: contig of 20960 bp in length 51330: gap of unknown length of 25551 bp in length unknown length contig of 97073 bp in length 4685: contig of 4685 bp in length 4785: gap of unknown length 9848: contig of 5063 bp in length 9948: gap of unknown length

pease validades cds. Tible gene, partial cds. PEI 14-MRR-2000 pease validades cds. Tible gene, partial cds. PEI 14-MRR-2000 pease complete cds. Tible gene, partial cds. PEI 25255 and PEES an	/rpt_type=dispersed /rpt_type=dispersed /rpt_type=dispersed /rpt_family="Alu" /rpt_type=dispersed	/ rpc_canty rpc_canty 1289. 12215 1289. 12215 rpc_family="Alu" rpc_tamily="Alu" rpc_family="Alu" rpc_tamily="Alu" rpc_family="Alu" rpc_family="Alu" rpc_family="Alu" rpc_family="Alu" rpc_family="Alu"	/rpc_type=clspersed 1407514295 /rpt_family="L1" /rpt_type=clspersed complement 11484815120) /rpt_family="Alu" /rpt_family="Alu" /rpt_family="Alu" /rpt_family="MER20" /rpt_family="MER20" /rpt_family="MER20" /rpt_family="Alu" /rpt_family="Alu" /rpt_family="Alu" /rpt_family="Alu" /rpt_family="Alu" /rpt_family="Alu" /rpt_family="Alu"	Complement (1649516633) /rpt_family="Alu" /rpt_fype=dispersed 1696017705 /rpt_fype=dispersed /rpt_fype=dispersed /rpt_fype=dispersed /rpt_fype=dispersed /rpt_fype=dispersed /rpt_fype=dispersed /rpt_fype=dispersed /rpt_fype=dispersed /rpt_fype=dispersed /rpt_fype=dispersed /rpt_fype=dispersed /rpt_fype=dispersed /rpt_fype=dispersed /rpt_fype=dispersed	/ rpt_tamily="Allu" / rpt_type=dispersed complement (20503. 20804) / rpt_tamily="Allu" / rpt_type=dispersed 2184422129 / rpt_tamily="Allu" / rpt_tamily="Allu" / rpt_type=dispersed 2291823184 / rpt_type=dispersed / rpt_type=dispersed / rpt_type=dispersed / rpt_type=dispersed / rpt_type=dispersed / rpt_type=dispersed / rpt_type=dispersed / rpt_type=dispersed / rpt_type=dispersed / rpt_type=dispersed / rpt_type=dispersed / rpt_type=dispersed / rpt_family="Allu"
AP168787 AP168787 Home sapiens vanilloid arecgior gene, partial sequence; complete cds, TIP1 gene, partial cds, PASD genes, complete cds, TIP1 gene, partial cds, PASD AP168797 AP168797 AP168797 AP168797 AP168797 AP168797 Home sapiens (human) Home sapiens			region region region		
	AF168787 AP168787 AP168787 CTNS genes, complete cds; TIP1 gene, partial sequence; CTNS genes, complete cds; TIP1 gene, partial cds; P2X5b genes, complete cds; TIP1 gene, partial cds; P2X5b genes, complete cds; and HUMINAE gene, partial cds. AP168787 AP168787 AP168787 AP168787 Homo sapiens (human) Ho		rce 1.200237 / Organism="Homo sapiens" / Organism="Homo sapiens" / Mb_xref="taxon:9606" / Chromosome="17" / map="17p13" complement(<127738) / gene="vanilloid receptor" / note="coding sequence not determined, norvegicus vanilloid receptor subtype Accession Number AFO29310" / evidence=not experimental	/w//H//H//	

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137900 ---GGTGAGCTGAGATGACGCCATTGCACTCCAGCCTGGGCAACAAGAGCAAACTCTGC 137956
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                                                                                                                                                                                                                                                                                                                                           PRI 30-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (13-AUG-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (Dases 1 to 129625)
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Submitted (15-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 129625)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 129628)
Sulston, J.E. and Waterston, R.
                                                    137840 TCCCAGCTACTCGGGAGGCTGAGGCAGAGAATTGCTTGAACCCAGGAGGCAGAGTTGT
                          2381 TCCCAGCTACTCAGGAGGCTGAGGC-GGAGAATTGCTTGAACCCGGAAGGTGGAGGTTGT
                                                                                                          2440 TGCGGTGAGCTGAGATTGCACTTCCAGCCTGGGCAACAGGAGTAAAACTCCCC
                                                                                                                                                                                                                                                                                                                              ACO09301 129625 bp DNA linear PRI 30-6
Homo sapiens BAC clone RP11-62F14 from 2, complete sequence.
AC009301
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Drone,K., Leonard,S. and Doebber,A.
The sequence of Homo sapiens BAC clone RP11-62F14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                        AC009301.3 GI:7243885
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Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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Best Local Similarity 87.5%;
Matches 266; Conservative (
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Pred. No. 2.3e-32;
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6160.
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                              MAPPING INFORMATION: Mapping information for this clone was provided by Dr. John D. Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                             The clone sequenced to the left is RPI1-153B21, 200 bp overlap. Actual start of this clone is at base position 133171 of RPI1-153B21; actual end is at base position 129625 of RPI1-62F14. Location/Qualifiers
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (20-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, O., Wand-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williams, G., Williams, G., Williams, G., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Apr 28, 2002 this sequence version replaced gi:18449820.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4906: contig of 4906 bp in length 12370: contig of 1364 bp in length 12470: contig of 1364 bp in length 12470: gap of unknown length 12159: contig of 8989 bp in length 13615: contig of 12056 bp in length 13715: gap of unknown length 47492: contig of 13777 bp in length 69615: contig of 22023 bp in length 69615: contig of 22023 bp in length 69747: contig of 25023 bp in length 69747: contig of 25023 bp in length 121218: gap of unknown length 121218: contig of 25371 bp in length 121318: contig of 25371 bp in length 146590: contig of 25372 bp in length 166828: gap of unknown length 166828: contig of 21438 bp in length 168128: contig of 21438 bp in length 168128: contig of 21438 bp in length 16828: gap of unknown length 168128: contig of 21438 bp in length 16828: contig of 21438 bp in length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828: gap of unknown length 16828.
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gap of unknown length
contig of 26717 bp in length
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Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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Direct Submission
Submitted (20-JAN-2002)
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Direct Submission
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I (Dases I to 31886)

I (Dases I to 11886)

Muzny, D.M., Adame, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alabrooke, S. L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barton, J., Burket, C., Burch, B., Brown, M., Bryant, N.P., Barbaria, J., Benton, J., Burket, C., Burrell, K.L., Byrd, N.C., Chavez, D., Chen, G., Chen, R., Chen, R., Cavazos, S.R., Carkok, J., Chavez, D., Chen, G., Chen, R., Coyle, M.D., Dabthorne, S.R., David, R., Davis, C., Coyle, M.D., Dabthorne, S.R., David, R., Davis, C., Davis, C., Coyle, M.D., Dabthorne, S.R., David, R., Davis, C., Davy-Carroll, L., Didg, Y., Dinh, H.H., Duvis, C., Daye, Carroll, L., Ding, Y., Dinh, H.H., Duvis, C., Barch, D., Elago, N., Ford, J., Foster, P., Frantz, P., Garla, A., Garcia, A., Garner, T., Garcia, P., Manilton, K., Harris, C., Harris, C., Harris, C., Hart, M., Harlak, P., Hawes, A., Hernandez, J., Gacta, A., Hogues, M., Holloway, C., Hollins, B., Jackson, E., Karlsson, E., Kally, S., Khan, W., Holloway, C., Hollins, B., Jackson, E., Karlsson, E., Kally, S., Khan, W., Martin, B., Lewis, L., Louseey, E., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Sodergien, R., Scott, G., Scott, G., Scott, G., Scott, G., Scott, G., Scott, G., Scott, G., Scott, G., Scott, G., Scott, G., Scott, G., Scott, G., Scott, G., Sc
                                                                                                                                                                                                                                                                                                                                                                                     104230 ATTTAATGGCTCAAAGGCCGGGAGCAGTGACCCATGCCTGTAATCCCAGCACTTTGGGAG 104171
                                                                                                                                                                                                                                                                         104170 GCCAAGGTGGGCAGATCACCTGAGGTCAGGAGTTCGAGACCAGCCTGGCTAACATGGTGA 104111
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Homo sapiens chromosome 3 clone RP11-372J10, WORKING DRAFT
SEQUENCE, 14 unordered pieces.
                                                                    2207 ATATAAAATACCCCGGCCAGGCACGGTGGCTCACGCCTGTAATCCCCAGCACTTTGGG-- 2264
                                                                                                                                                                                                        2265 ----AGGTGGGTGGATCACCTGAGGTCGGGAGTTCGAGACCAGCCTGACCAGCATGGTGG
                                                                                                                                                                                                                                                                                                                                             AACCCCCATCTCTACTAAAAACACAAAAATTAGCCGGGCGTGGTGGCACATGCCTGTAA
       7; Gaps
   0; Mismatches 44; Indels
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AC107422.3 GI:20335954
HTG: HTGS PHASE1; HTGS_DRAFT.
HOMO SADIEDS (human)
Matches 252; Conservative
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242665 ATTTAATGGCTCAAAGGCCGGGAGCAGTGACCCATGCCTGTAATCCCAGCACTTTGGGAG 242724
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                                                                                                                                                                                                                                           7; Gaps
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221745 221844: gap of unknown length
221845 267827: contig of 45983 bp in length
267828 267927: gap of unknown length
267928 318586: contig of 50659 bp in length.
Location/Qualifiers
1. 318586
/ Organism="Homo sapiens"
//mol_type="genomic DNA"
//db_xref="leaxon:9606"
//chromosome="3"
//clone="RP11-372J10"
                                                                                                                                                                                                                                           44; Indels
                                                                                                                                                                                                         Query Match 7.9%; Score 198.6; DB 2; Best Local Similarity 83.2%; Pred. No. 2e-32; Matches 252; Conservative 0; Mismatches 44;
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         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Add10849 Human STA Ad113819 Osteoarth Ad13819 Osteoarth Ada48556 Human Not Ad687336 Human GPC Ad689008 Human GGC AA68958 Human GGT AA69958 Human and AAG19183 Human sof AAG19183 Human sof Ab65090 DNA encod Ab669090 DNA encod Ab669090 DNA encod Ab669148 Human sof Ab669090 DNA encod Ab669148 Human can Ad653148 Human can

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AAK71814 AAI62921

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AAK87568

ABA07221 AAK89858

ADQ19183

ABK83497 ADQ18538 ABK69090

227968 110665

ABD33145 ADP65796 ACH36634

270150 463 89625

73723

ACN45194 ACN44082 ACN44410

71048 91760

ALIGNMENTS

Acn45194 Human gen Acn44082 Human gen Acn44410 Human gen

The invention provides nucleic acid markers of prostate, breast and bladder cancer. The markers are indicators of malignant transformation of prostate, breast and bladder tissues and are diagnostic of the potential for metastatic spread of malignant prostate tumours. The nucleic acid can also be used as targets for therapeutic intervention in prostate cancer, benign prostatic hyperplasia (BPH), bladder cancer or breast cancer. The markers may be used to design specific probes and primers, for the rapid Nucleic acid marker; biomarker; tumour; prostate cancer; bladder cancer; benign prostatic hyperplasia; BPH; breast cancer; human; immunodetection; Novel RNA biomarkers for diagnosis, prognosis and management of prostate, breast and bladder cancer. Prostate disease marker UC Band #28 splice variant Veltri RW; Claim 1; Page 184-186; 191pp; English. AAZ87584 standard; DNA; 2506 BP 98US-00097199 99WO-US013151 O'hara SM, Ralph D, diagnosis; PCR primer; 88. (first entry) WPI; 2000-116557/10. (UROC-) UROCOR INC P-PSDB; AAY59296 Homo sapiens. 11-JUN-1999; 12-JUN-1998; W09964631-A1 19-APR-2000 16-DEC-1999 AAZ87584; An G, RESULT 1 AAZ87584

Aa287583 Prostate
Aa964000 Biomarker
Aav5683 Human pro
Aax86018 Prostate,
Aa287503 Prostate,
Aa67503 Prostate,
Ad659380 Human can
Ad65292 Human imm
Abal5481 Human ner
Abal5481 Human ner
Abal5481 Human ner
Abal5481 Human imm
Aax71816 Human imm
AaX71816 Human imm
AaX718113 Human imm

AAX26018 AAZ87503 AAS03722 ADQ59380

AAZ87583 AAS04000 AAV16883

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AAZ87584 AAS04001

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ABA15481 ABA15482

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AAK71816 AAK73113

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AA162923

AAK87584

Aaz87584 Prostate Aas04001 Biomarker

Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2000s:* geneseqn2001as:* geneseqn2001bs:* geneseqn2002as:* geneseqn2002bs:*

Geneseq_16Dec04:*

Database

Minimum DB Maximum DB

Searched:

geneseqn1980s:* geneseqn1990s:*

geneseqn2003as:* geneseqn2003bs:* geneseqn2003cs:* geneseqn2003ds:* geneseqn2004as:* geneseqn2004bs:*

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SUMMARIES

Aai 62923 Human gen Abz 74674 Secreted Abz 68196 Human sec Aak 73099 Human imm

ABZ74674 ABZ68196 AAK73099

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analysis of prosterie, bladder or breast bloopsy samples. The probes and primers may also be used for in situ hybridization or in situ PCR detection and diagnosis. They may also be used to identify and isolate full length gene sequences form various DNA libraries. Antibodies against the polypeptide products of the markers can be used to treat prostate cancer. bladder cancer or breast cancer. The encoded proteins may be used to detect antibodies. The proteins and antibodies can be used in immunodetection methods for detecting or quantifying the cancers and for clinical diagnosis of these cancers. The antibodies may also be used for radioimaging to quantify and localize the encoded proteins	Sequence 2506 BP; 822 A; 519 C; 446 G; 718 T; 0 U; 1 Other;	Query Match 100.0%; Score 2505.6; DB 3; Length 2506; Best Local Similarity 100.0%; Pred. No. 0; Matches 2506; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 GACCTTAAATATATCGAGGTGGCTAATTGATGTATAATAATTTACAAAATTATTCTTCTA 60 	TTGCTACAGAGCTACAATTTCAATTTACAGTAGGCCACCATGAGGGCCTTCTTAAGGAACC	61 TIGCTACAGAGCTACAATTTACAGTAGGCCACCATGAGGGCCTTCTTAAGGAACC 120	121 AGAAATATGAGGATATGCACAATATTATTCACATTTTACAGATCAGAAAATTGAGGCACA 180	121 AGAAATATGAGGATATGCACAATATTATTCACATTTTACAGATCAGAAAATTGAGGGCACA 180	GATTAAGTAACTTCCCAAGGCTACCAGGCATTCTAGCTCCAGAAACTGTGCTCTTACCAT	81 GATTAAGTAACTICCCAAGGCTACCAGGCATICTAGCTCCAGAAACTGTGCTCTTACCAT	241 TCTGCTACAAGGTATTTCGAAAAAAGAAAAGGTAAAAGGTCAAAAGGCAACAGAGT 300 	TCATTGATTATTCCATAGAACAGTCACACGTGCAATTCTCACACCCTTGCAGACACACT	301 TCAITGAITAITCCAIAGAACAGTCACAGCAATTCTCACACCCTTGCAGACACACT 360	361 IGACCATGAAAGGTTCCTCAATGAAAIGTTCCTCATTATCTTCAGAAGCCATATTATTCA 420	361 IGACCATGAAAGGTTCCTCAATGAAATGTTCCTCATTATCTTCAGAAGCCATATTATTCA 420	421 CATTGACTTTGCAGTTAACTCAGACCCTAGGTCTGGAATGCTGTCTTCTCTACCTATCCA 480	CATTGACTITIGCAGTTAACTCAGACCCTAGGTCTGGAATGCTGTCTTCTCTATCTA	481 AAACTATACATCACACATATAAACTCTCAGCCCTGCAAAAGAAAAA 340 481 AAACTATACATCCACAGATCATATAAACTCTCAGCCCTGCTGCAAAGCCTTTCCAGAAAA 540	541 ATAAAAHGGTTGAAAAGGCAATTCTGCTACCAATGACTGTTTAAGCCCAAGCAAG	541 ATAAAATGGTTGAAAAGGCAATTCTGCTACAATGACTGTTTAAGCCCAGCCAAGTAAC 600	601 IGAACCATTCCAACTTCAATTTACTTATGAAAAGAATTTGATGATGATGAGGAGGTTATTTC 660	601 rgaaccarrccaacrrcaarrracrrargaaagaarrrgargargragaggrrarrc 660	661 AATTCTAAAATACAAACCCATGTTGATCTTTCTCAATCTTGGACTCATAGATTATTATCT 720	661 AATTCTAAAATACAAACCCATGTTGATCTTTCTCAATCTTGAACTCATAGATTATTATCT 720	721 AITAICICAAITIAGITIGITATITAICCIAGIGGGCCAIDAAAACIACCACAIGIGIT 780	721 ATTATCTCAATTTAGTTTTTTTTTTTTTGGGCCATTAAAACTACCACATGTGTT 780	81 TCTGTCTCTCCATTAGTCAATAACTAACGAGCAATTAGTAAGCCATGTGCCAGAT 84	781 TCTGTCTCTCCATTAGTCAATAACTAAACTAACGAGCAATTAGTAAGCCATGTGCCAGAT 840	
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δ	1321	TGGTGGTGCTTTAAAAAGATATTAATAGATAATATGAAAATCTCCATCTCAAAATAATG 1380
QQ	1321	TGGTGGTGTTTTAAAAAGATATTAATAGATAATATGAAAATCTCCATCTCAAAAATAATG 1380
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                                                                                Claim 2; Col 121-125; 78pp; English
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              2001-289849/30.
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                                TGCTCCCAGACCAAGGCACTGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biomarker UC band 28 #3, used in diagnosis and prognosis of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prostate; breast; bladder; cancer; biomarker; probe; diagnostic; benign prostatic hyperplasia; BPH; therapeutic; human; ss.
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/*tag= a
/product= "Prostate cancer marker protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                       AAS04001 standard; cDNA; 2505
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New nucleic acids as biomarkers and targets useful for detecting, diagnosing, prognosing, and in developing treatments for prostate, breast and bladder cancer.
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                                                                                                                                                                                                                    The sequence represents nucleic acid biomarker UC band 28 #3, used in detection of prostate, breast and bladder cancer. Biomarker nucleic acid sequences can be used as hybridiseation probes and primers that specifically hybridise to prostate cancer, benign prostatic hyperplasia (BPH), bladder cancer or breast cancer markers. Proteins encoded by the nucleic acid markers can be used to produce antibodies for the detection of prostate, breast or bladder cancer. The nucleic acids can be used as targets for therapeutic intervention in these diseases, in the identification and isolation of full-length gene sequences, including regulatory elements for gene expression, from genomic human DNA libraries, as hybridisation probes for screening genomic human DNA libraries. The kits comprising the nucleic acid sequences are useful for
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720 780 840 840 960 960 1020 1140 1140 1130 1130 11440 1150 1150 1150 1150 1150 1150 11	1741 ACCCRAGAGNITGCTACAAATCTTCTGAAAGGTTCCAATGGCTTCAGGCTAAGAGAAATTTGTTCAAAAATTAGCAGAAAAAAGAAATTAGCTTCAAAAATTAGCAGAAAAAAAA	RESULT 3 AAZ87583 ID AAZ87583 ID AAZ87583 XX AC AAZ87583; XX XX XX XX XX XX XX XX XX XX XX XX XX
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The invention provides nucleic acid markers of prostate, breast and bladder cancer. The markers are indicators of malignant transformation of prostate, breast and bladder tissues and are diagnostic of the potential for metastatic spread of malignant prostate tumours. The nucleic acid can also be used as targets for therapeutic intervention in prostate cancer. The markers may be used to design specific probes and primers, for the rapid analysis of prostate, bladder or breast cancer. The markers may also be used for in situ hybridization or in situ PCR detection and diagnosis. They may also be used to insitu ya nisolate the polypeptide products of the markers can be used to treat prostate the polypeptide products of the markers can be used to treat prostate cancer. bladder cancer or breast cancer. The encoded proteins may be used concert. bladder cancer or breast cancer. The encoded proteins may be used to immunodetection methods for detecting or quantifying the cancers, and for clinical diagnosis of these cancers. The antibodies may also be used for radioinmaging to quantify and localize the encoded proteins
                                                                                                                                                                                                                                      Novel RNA biomarkers for diagnosis, prognosis and management of prostate, breast and bladder cancer.
                                                                                                                            O'hara SM, Ralph D, Veltri RW;
                                                                                                                                                                                                                                                                                                        Claim 1; Page 182-183; 191pp; English.
99WO-US013151
                                          98US-00097199
                                                                                                                                                                     WPI; 2000-116557/10.
P-PSDB; AAY59295.
                                                                                 (UROC-) UROCOR INC
11-JUN-1999;
                                          12-JUN-1998;
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Sequence 2088 BP; 740 A; 406 C; 337 G; 604 T; 0 U; 1 Other;

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	Similarity 99.	ACCTTAAAT ACCTTAAAT	TTGCTACAGAGCTA TGCTACAGAGCTA	GAAATATGA GAAATATGA	ATTAAGTAA ATTAAGTAA	CTGCTACAA CTGCTACAA	CATTGATTA 	GACCATGAA GACCATGAA	ATTGACTTT ATTGACTTT	AACTATACA
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CCTTATGAGCAGGAAGAGGCTGTTTGAGAACCATTTACTTAGCAGAACCACATAT 1620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence represents nucleic acid biomarker UC band 28 #2, used in detection of prostate, breast and bladder cancer. Biomarker nucleic acid sequences can be used as hybridisation probes and primers that
                                                                                                                                                                                                    CTAACCATCTGAAGAAACTTCCCAAGTGTAAGACTCTGCCATTAAAACATTACCGAGA 1978
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                                                                                                                                                                                                                                                                                                                       Biomarker UC band 28 #2, used in diagnosis and prognosis of cancer.
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benign prostatic hyperplasia; BPH; therapeutic; human; ss.
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specifically hybridise to prostate cancer, benign prostatic hyperplasia (BPH), bladder cancer or breast cancer markers. Proteins encoded by the nucleic acid markers can be used to produce antibodies for the detection of prostate, breast or bladder cancer. The nucleic acids can be used as targets for therapeutic intervention in these diseases, in the identification and isolation of full-length gene sequences, including regulatory elements for gene expression, from genomic human DNA libraries, as hybridisation probes for screening genomic human DNA libraries. The kits comprising the nucleic acid sequences are useful for
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                                                                     901 AGTAACTAGTGAAATGTTCAAGTCATGCCTGAGTCAAGAGTTGAGGAGACACTTACAATGT
                                                                                                                         GTAATGGAAACCAAGGAAAGTGAAACTTTGGATAAGTGGGGACTAGTGTTTTTATATATT
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            GTAATGGAAACCAAGGAAAGTGAAACTTTGGATAAGTGGGGACTAGTGTATTTATATT
                                                                                                                                                                            1021 TAATTGATTTCTGACTCTATCATTGGCCTCCAAACACACAGATTGTGTTTTTCTTTGGTTTT
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                                                                                                                                                                                                                                            1081 GTTTTCTTCACTATGGGATCTTCTGTGCCCAGCACAGTGCCTGACACATAGAAACAATC
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nucleic acid segments shown in AAV16881 to AAV16885, AAV16890 to
CC AAV16903, AAV26351 and AAV26352 which can act as human prostate cancer
AAV16903, AAV26351 and AAV26352 which can act as human prostate cancer
CC Markers are provided in the specification. It also provides methods for
identifying markers for human prostate cancer and for detection of
prostate cancer cells. The markers can be identified by amplifying human
CC prostate RNA to provide nucleic acid amplification products, separating
CC the products and identifying those RNA that are differentially expressed
CC between human prostate cancers versus normal or benign human prostate.
CC acid in a sample can be detected by detecting a nucleic
CC acid in a sample, the nucleic acid being a prostate cancer marker.
CF Prostate cancer cells in a sample. Antibodies against the protein
CC for prostate cancer cells in a sample. Antibodies against the protein
CC encoded by the marker nucleic acid fragments, inhibitors of the protein
CC and oligonucleotides antisense to the markers can be used for the
CC diagnosis of human prostate cancer. The antibodies can also be used for the
CC diagnosis of human prostate cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This represents a marker sequence for human prostate cancer. Isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1686 ACAACGACACATTCAGGAGTTAAATATTTTTCATCAAACATTGGATTTTTCCTTAACGCT
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                                                                                          Prostate cancer; human; marker; diagnosis; treatment; probe;
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Pred. No. 1.3e-135;
0; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human prostate cancer marker - useful for human prostate cancer.
Human prostate cancer marker UC Band #28.
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1986 CAAACAGTCTTT -- CTICCTTIGTCGTGTTTC-TTGCTCCCAGACCAAGG------CACT 2036
                                                                                                The invention relates to methods for diagnosing prostate cancer or benign prostatic hyperplasts cells in a biological sample. The method uses oligonucleotide probes specific for marker genes associated with tumour differentiation and progression in Reverse Transcription Polymerase Chain for detecting and monitoring the progression of benign prostate chain for detecting and human prostate cancer (the most prevalent form of and a major cause of death in males) prior to the tumor undergoing metastasis, therefore allowing the optimal method of treatment to be determined before the condition becomes life threatening. The present sequence represents a claimed marker gene fragment
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                                                                                                                                                                                                                                                                                                                                                               Sequence 757 BP; 228 A; 190 C; 147 G; 192 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 25.0%; Score 626.2; DB 2; Best Local Similarity 94.6%; Pred. No. 1.3e-135; Matches 716; Conservative 0; Mismatches 28;
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                                                                                                                                                                    CAAACAGTCTTT - - CTTCCTTTGTCGTGTTTC- TTGCTCCCAGACCAAGG-----CACT
                          TTCTTTCCAAAAGGAACTCTAGAAGACCAAATGCCCCGAGTTAAGAACATCAAAACTAAC
                                                                                                                                                                                              GAACTCTAATTGGACCACCCTGAAGCTTAGGA-CTACCAGCCATACAAATAGTAAAACTCT
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                                                                                   CATCTGAAGAAACTTCCCAAGTGTAAGACTCTGCCATTAAAACATTACCGAGAGGGGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention provides nucleic acid markers of prostate, breast and bladder cancer. The markers are indicators of malignant transformation of prostate, breast and bladder tissues and are diagnostic of the potential for metastatic spread of malignant prostate tumours. The nucleic acid can also be used to therapeutic intervention in prostate cancer. The markers may be used to design specific probes and primers, for the rapid analysis of prostate, bladder or breast biopsy samples. The probes and cancer. The primers may also be used for in situ hybridization or in situ PCR offiction and diagnosis. They may also be used to identify and isolate thil length gene sequences form various DNA libraries. Antibodies and cancer, bladder cancer of the markers can be used to treat prostate to detection methods for the markers can be used to treat prostate cancer, bladder cancer or breast cancer. The encoded proteins may be used to detection methods for detecting or quantifying the cancers, and for climical diagnosis of these cancers. The antibodies may also be used for radioimaging to quantify and localize the encoded proteins
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                                                                                                                                                                                                                                                                                             Nucleic acid marker; biomarker; tumour; prostate cancer; bladder cancer; benign prostatic hyperplasia; BPH; breast cancer; human; immunodetection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel RNA biomarkers for diagnosis, prognosis and management of prostate, breast and bladder cancer.
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                                                                                                              AAZ87503 standard; cDNA; 757
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                                                               RESULT 7
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8 셤 ò 셤 ò

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PT New nucleic acids as biomarkers and targets useful for detecting,
T diagnosing, prognosing, and in developing treatments for prostate, breast
XX
PS Claim 2; Col 79; 78pp; English.
XX
CC detection of prostate, breast and bladder cancer. Biomarker nucleic acid
detection of prostate, breast and bladder cancer. Biomarker nucleic acid
sequences can be used as hybridisation probes and primers that
cC Geptifically hybridiset cancer markers. Proteins encoded by the
nucleic acid markers can be used to produce antibodies for the detection
of prostate, breast or bladder cancer. The nucleic acid as
cC targets for therapeutic intervention in these diseases, in the
identification and isolation of full-length gene sequences, including
cc targets for therapeutic intervention in these diseases, including
cc targets for therapeutic on probes for screening genomic human DNA
cc libraries as hybridiaation probes for screening genomic human DNA
cc libraries. The kits comprising the nucleic acid sequences are useful for
cc detecting bladder, breast or prostate cancer cells in a biological sample
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Query Match
Score 626,2; DB 4; Length 757;
Best Local Similarity 94.6*; Pred. No. 1.3e-135;
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                                                                                                                                                                                                                    1746 AGAGATTGCTACAAATCTTCTGAAGGGTCTCAATGGCTTCAGGCTAAGAAGAGATTTCTC
                                                                                                                                                                                                                                                                         61 AGAGATTGCTACAAATCTTCTGAAGGGTCTCAATGGCTTCAGGCTAAGAAGAGATTTCTC
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                                                                                                            1686 ACAACGACACATTCAGGAGTTAAATATTTTTCATCAAACATTGGATTTTTCCTTAACGCT
                                                                                                                                                               1 ACAACGACACTTCAGGAGTTAAATATTTATCATCAAACATTGGATTTTTCCTTAACGCT
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Query Match 25.0%; Score 626.2; DB 4; Length 757; Best Local Similarity 94.6%; Pred. No. 1.3e-135; Matches 716; Conservative 0; Mismatches 28; Indels 13; Gaps
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The present invention describes human cancer-associated (CA) nucleotide sequences (I). Also described: (1) an expression vector comprising (I); (2) a host cell comprising (I) or the expression vector; (3) a microarray for detecting a CA nucleic acid; (4) an isolated polypeptide encoded within an open reading frame of a CA sequence; (5) an isolated antibody, or its antigon binding fragment, that binds to the above polypeptide; (6) a hybridoma that produces the monoclonal antibody and a pharmaceutical composition comprising the antibody and a pharmaceutical expipant; (8) a kit for detecting or diagnosing cancer cells, comprising the above (monoclonal) antibody or polymucleotide that selectively (1) apprindises to any of the polymucleotide sequences mentioned above; (9) methods for diagnosing cancer or for detecting the presence or absence of cancer cells in an individual; (10) a method for inhibiting growth of cancer cells in an individual; (11) a method for inhibiting growth of cancer cells in an individual; (12) an electronic library comprising the polymucleotide or polypeptide, or their fragments, comprising the polymucleotide or polypeptide, or their fragments, comprising the polymucleotide or polypeptide, or their fragments, comprising the polymucleotide or polypeptide, or their fragments, comprising the polymucleotide or polypeptide, or their fragments, compressing cancer associated with expression of a polypeptide or the attibody in a test cell or serum sample; (15) a cattivity of a CA protein encoded by the above nucleic acid molecule; and (16) a method for treating cancers (1) has cytostatic acid molecule; and cathod of the present invention can be used for treating cancer, especially lymphomas. They may also be used in an treating cancer in the receptor antiagonist; and methods of the present invention can be used for preventing cancer, especially lymphomas. They may also be used in the exemplification of the present invention. Note: The sequence dors the prevented that the parent invention of the prese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New cancer-associated nucleic acid for diagnosing, preventing or treating cancer (e.g. lymphoma) or for screening agents that may be used for treating or preventing cancer.
                                                                                                                                                                                                                                                                                                                                                   human, cancer-associated gene, cancer-associated protein, cytostatic, gene therapy, vaccine, tyrosine kinase antagonist;
G-protein coupled receptor antagonist; cancer; lymphoma; gene, ds.
                                                                                                                                                                                                                                                                                                         Human cancer-associated (CA) gene sequence SEQ ID NO:16.
                      721 AGGAGGCTGAGGCGGAGAATTGCTTGAACCCGGAAGG 757
2393 AGGAGGCTGAGGCGGAGAATTGCTTGAACCCGGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 16; SEQ ID NO 16; 143pp; English.
                                                                                                                                                               ADQ59380 standard; DNA; 299598
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                                                                                                           2168 ATCTGTGTATTTTCTATAGATGTTTACTAGGCGTTTGTTATAAAAATACCCCGGCCAG 2227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated cancer associated nucleic acids comprising at least 10 contiguous nucleotides, useful for diagnosing, preventing and/or treating cancers such as leukemia and lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to cancer associated sequences (ADQ97025-ADQ98004). The sequences are useful for the diagnosis, prevention and/or treatment of cancer, such as leukemia and lymphoma. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formate directly from WIPO at
                                  Sequence 299598 BP; 92218 A; 54563 C; 55801 G; 95585 T; 0 U; 1431 Other;
                                                                                                                                                                                                                                                                                                          2402 AGGC-GGAGAATTGCTTGAACCCGGAAGGTGGAGGTTGTTGCGGTGAGGTTGCAC
                                                                                                                                                           GCACGCTGCCCCTGTAATCCCAGCACTTTGGGAGGT-----GGGTGGATCACCT
                                                                                                                                                                                                          2282 GAGGTCGCGAGTTCGAGCCAGCCTGACCAGCATGGTGGAACCCCCATCTCTACTAAAAA
                                                                                                                                                                                                                                                         2342 CACAAAAATTAGCCGGGCGTGGTGGCACATGCCTGTAATCCCAGCTACTCAGGAGGCTG
                                                                                     Gaps
                                                         Query Match 7.6%; Score 190.6; DB 12; Length 299598; Best Local Similarity 78.4%; Pred. No. 2.1e-33; Matches 269; Conservative 0; Mismatches 64; Indels 10; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Human; ds.
                                                                                                                                                                                                                                                                                                                                                                      241040 CATTGCACTCCAGCCTGGGCAACAAGAGCAAAACTCCATCTCA 240998
                                                                                                                                                                                                                                                                                                                                                          2461 TATTGCACTCCAGCCTGGGCAACAGGAGTAAAACTCCCCCCCA 2503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cancer associated sequence HD09-008, SEQ ID 500.
obtained in electronic format directly from WIPO at
           ftp.wipo.int/pub/published_pct_sequences.
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136836 ATAAATATCTCGGCCAGGCGTGGTGGTCTCACTCTGTAAATCCCCAGCACTTTGGGAGGCCA 136777
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Sequence 215974 BP; 56601 A; 42897 C; 46516 G; 65586 T; 0 U; 4374 Other;
                                                                                                                         2211 AAAAATACCCCGGCCAGGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGG-----
                                                                                                                                                                                                         2265 AGGTGGGTGGATCACCTGAGGTCGGGAGTTCGAGACCAGCCTGACCAGCATGGTGGAACC
                                                                                                                                                                                                                                   136776 AGGIGGGGGATCACCTGAGGTCGGCAGTTCAAGACCAGCCTGACCAACATGG-AGAAAC
                                                                                                                                                                                                                                                                                                                   AGCTACTCAGGAGGCTGAGGC-GGAGAATTGCTTGAACCCGGAAGGTGGAGGTTGTTGCG
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                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene thexapy; vaccine; metastasis; ds.
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                                         DB 12; Length 215974;
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                                      Score 186.8; DB 1
Pred. No. 1.4e-32;
                         7.5%; Scc. No. 1...
83.3%; Pred. No. 1...
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2000US-0214886P.
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2000US-0186350P.
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                                                                             Matches 250; Conservative
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2000US-025268P.
2000US-022547P.
2000US-022547P.
2000US-0225757P.
2000US-0225758P.
2000US-0225758P.
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2000US-0229287P.
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2000US - 024929P.
2000US - 0249300P.
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2000US-0251988P.
2000US-0256719P.
2000US-0251479P.
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    08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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08-NOV-2000;
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Rosen CA, Barash SC, Ruben SM

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 40104; 3071pp + Sequence Listing; English.

ANK54951 to AAK64702 encode the human immune/haematopoietic antigen (1)
amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
example, they may be used to treat disorders associated with decreased
contession by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
cuplement the patients own production of (I). Additionally, (I)
cuplement the patients own production of (I) additionally, (I)
cuplement the patients and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic-derived cells. AAK64703
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK54950 and AAM82169
represent sequences used in the exemplification of the present invention

Sequence 2680 BP; 723 A; 594 C; 630 G; 733 T; 0 U; 0 Other;

Query Match

7.4%; Score 186.4; DB 4; Length 2680;

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                                                                                                                          1191 AGGCCAAGGTGGGCGGATCACCTGATGTCAGGAGTTCGAGACCAGCCTGACCAACATGG-
                                                                            AATCCCAGCTACTCAGGAGGCTGAGGC-GGAGAATTGCTTGAACCCCGGAAGGTGGAGGTT
                                               2205 TTATATAAAAATACCCCGGCCAGGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGG
                                                                                                           -----AGGTGGGTGGATCACCTGAGGTCGGGAGTTCGAGACCAGCCTGACCAGCATGGT
                                                                                                                                                                    2319 GGAACCCCCATCTCTACTAAAAACACAAAAATTAGCCGGGCGTGGTGGCACATGCCTGT
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                    11;
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                   Indels
   Pred. No. 4.3e-33;
0; Mismatches 36;
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2000US-019123P.
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2000US-0220963P.
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    84.68;
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Best Local Similarity 84.6
Matches 259; Conservative
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24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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30-JUN-2000;
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07-JUN-2000;
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The intention retails to hovel genes (Aballuda-Aballuda) and proteins medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.

The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and covarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic ansemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy, and (f) infectious diseases such as wiral, bacterial, fungal and parasitic infectious diseases avoid as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel genes (ABA11004-ABA21534) and proteins
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                                                                                                                                                                                                                  3624 ATCACCTGAGGTCGGGAGTTCGAGACCAGCCTGACCAACATGG-AGAAACGACATCTCTA
                                                                                                                                2221 CGGCCAGGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGG-----GAGGTGGGTGG
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                                 Sequence 5788 BP; 1326 A; 1585 C; 1382 G; 1495 T; 0 U; 0 Other;
                                                                Length 5788;
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                                                                7.4%; Score 186.4; DB 5; Length 87.2%; Pred. No. 5.6e-33; ative 0; Mismatches 26; Indels
from WIPO at ftp.wipo.int/pub/published_pct_sequences
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2000US-0180628P.
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2000US-0186350P.
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2000US-019131P.
2000US-0198123P.
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                                                                                 Best_Local Similarity 87.2
Matches 253; Conservative
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25-SEP-2000;
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2000US-0249245P-2000US-0249245P-2000US-0249267P-2000US-024929P-2000US-0249300P-2000US-025186P-2000US-0251868P-2000US-0246523P.
2000US-0246524P.
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Rosen CA, Barash SC, Ruben (HUMA-) HUMAN GENOME SCI INC

WPI; 2001-541565/60

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cance and metastases.

cancers

Disclosure; SEQ ID NO 7813; 1701pp + Sequence Listing; English

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The mucleic acids, proteins, antibodies and (ant)agonists are useful in the adagnosis, treatment and prevention of: 13 cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune cancers e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing (e) neurological diseases such as wycardial anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of

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2000US-0225268P.
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2000US-0225477P.
2000US-0225757P.
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2000US-0227182P-

2000US-0227182P-

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the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                              ATCACCTGAGGTCGGGAGTTCGAGACCAGCCTGACCAGCATGGAGCCCCCATCTCTA
                                                                                                                                                                                                                                                                                                   CTAAAAACACAAAAAATTAGCCGGGCGTGGTGGCACATGCCTGTAATCCCCAGCTACTCAG
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                                                                                                                         11; Gaps
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                                                    Sequence 5788 BP; 1326 A; 1585 C; 1382 G; 1495 T; 0 U; 0 Other;
                                                                                      DB 5, Length 5788;
                                                                                    Query Match 7.4%; Score 186.4; DB 5; Length Best Local Similarity 87.2%; Pred. No. 5.6e-33; Matches 253; Conservative 0; Mismatches 26; Indels
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AAK87584/c
ID AAK87584 standard, DNA, 14417 BP.
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2000US - 018635P
2000US - 0189076P
2000US - 0198123P
2000US - 0205457P
2000US - 0205467P
2000US - 0214886P
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02 - MAR - 2000;
17 - MAR - 2000;
11 - MAR - 2000;
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07 - UNN - 2000;
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08-NOV-2000;
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17-NOV-2000;
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Ruben SM

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 42396; 3071pp + Sequence Listing; English.

cartivity, and can be used in AMM812170 to AAM81921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diagnosis may be used in the prevention, diagnosis and treatment of diagnosis and treatment of diagnosis and treatment of diagnosis and treatment of diagnosis and treatment of diagnosis and treatment of diagnosis and treatment of diagnosis and treatment of diagnosis or deletions in a patient's genome complex they may be used to treat disorders associated with decreased that affect the activity of (I) by expression proteins or to supplement the patients own production of (I). Additionally, (I) collaboration of the secreted (I), by inserting the polynucleotides may be used to produce the secreted (I), by inserting the collaboration diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 cancers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK54921 to AAK54503 and AAM82169 represent sequences used in the exemplification of the present invention AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

Sequence 14417 BP; 3988 A; 3462 C; 3356 G; 3611 T; 0 U; 0 Other;

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AATCCCAGCTACTCAGGAGGCTGAGGC-GGAGAATTGCTTGAACCCCGGAAGGTGGAGGTT
                                                                                                                                                                                                        GTTGCGGTGAGCTGAGATTGCACTATTGCACTCCAGCCTGGGCAACAGAGAGTAAAACTCC
                                                                                                                                                                                                                                                 2474 GTTGCAGTGAGCTGAGATTGCACCACTGCACCCCAGCCTGGGCAATAAGAGTGAAACTCC
                                              2205 ITATATAAAAATACCCCGGCCAGGCACGGTGGCTCACGCCTGTAATCCCCAGCACTTTGGG
                                                                   2710 Titiaaaaadaaaaaccectececcecteccectectectecaaccaccattece
                                                                                          -----AGGTGGGTGGATCACCTGAGGTCGGGAGTTCGAGACCAGCCTGACCAGGATGGT
                                                                                                       2650 AGGCCAAGGTGGGCGGATCACCTGATGTCAGGAGTTCGAGACCAGCCTGACCAACATGG-
                                                                                                                                          2319 GGAACCCCCATCTCTACTAAAAACACAAAAATTAGCCGGGCGTGGTGGCACATGCCTGT
                                                                                                                                                       Human, immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26628
Length 14417;
                       Indels
7.4%; Score 186.4; DB 4;
84.6%; Pred. No. 7.4e-33;
7ative 0; Mismatches 36;
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2000US-0205515P,
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                       Matches 259; Conservative
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            Similarity
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16-MAR-2000;
11-MAR-2000;
18-APR-2000;
19-MAY-2000;
28-JUN-2000;
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30-JUN-2000;
07-JUL-2000;
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Rosen CA, Barash SC, Ruben SM,

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis

Disclosure, SEQ ID NO 26628; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polymucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
c supplement the patients own production of (I). Additionally, (I)
c polynucleotides may be used to produce the secreted (I), by inserting the
nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastesses of haematopoietic-derived cells. AAK64703
c to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54951 to AAK64950 and AAM82169
crepresent sequences used in the exemplification of the present invention

Sequence 14417 BP; 3611 A; 3356 C; 3462 G; 3988 T; 0 U; 0 Other;

Query Match

DB 4; Length 14417; 7.4%; Score 186.4;

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2205 TTATATAAAAATACCCCGGCCAGGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGG 2264
Best Local Similarity 84.6%; Pred. No. 7.4e-33;
Matches 259; Conservative 0; Mismatches 36; Indels 11; Gaps
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 3311
LENGTH: 2506
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99.5%; Pred. No. 0;
ive 1; Mismatches
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Patent No. 6812339
GENERAL INFORMATION:
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Best Local Similarity 99.5°
Matches 2494; Conservative
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ORGANISM: Human
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US-09-949-016-15053
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                                           ACCTTATGAGCAGGAAGAGGGTGTTTGAGAACCATTTACTTAGCAGAACCACATA
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RESULT 3

US-09-949-016-15053

Sequence 15053, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PELLING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOCTHARE: PSELSEQ for Windows Version 4.0

LENGTH: 6507
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                                     ATCACATTCTTTCCAAAAGGAACTCTAGAAGACCAAATGCCCCGAGTTAAGAACATCAAA
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                                                                                                                                                                                                                                                                                                                                                 Sequence 83, Application US/09097199
; Batent No. 6218529
; GENERAL INFORMATION:
; APPLICANT: A., Gang
; APPLICANT: O'Hara, S. Mark
; APPLICANT: O'Hara, S. Mark
; APPLICANT: Veltri, Robert
; TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
; TITLE OF INVENTION: BYOGNOSIS AND MANAGEMENT OF PROSTATE DISE;
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOld, White & Durkee
; STREET: ALOUGH ON 4433
; CITY: Houston
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STATE: Texas

COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,199
                                                                                                                                                                FILING DATE:
CLASSIPICATION NUMBER: US/09/09/199
PILING DATE:
PRIOR APPLICATION DATA:
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 08/692,787
FILING DATE: 31-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Nakashima, Richard A.
REGISTRATION NUMBER: P-42,023
REFERNEK/DOCKET NUMBER: URC::018
TELEPHONE: (512) 418-3000
TELEPAX: (512) 418-3000
TELEPAX: (512) 44-7577
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 2087 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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; LOCATION: 99..503
US-09-097-199-83
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US-09-097-199-3
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                                           1621 TTTAGACACTTCCCTGCATTAACTGCACAAACAATATGTTTGCAAACTTGTT-GATCAAC 1679
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Patent No. 5882864

GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: O'Hara, S. Mark
APPLICANT: O'Hara, S. Mark
APPLICANT: Walph, David
APPLICANT: Weltri, Robert
ITILE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
ITILE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: House of Mark Address
CITY: House of Mark Address
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/692,787
FILING DATE: Concurrently Herewith
CLASSIFTCATION: 514
ATTONEY/AGENT INFORMATION:
NAME: COCACET, Timothy S.
REGISTRATION NUMBER: 38,414
RESPENCE/DOCKET NUMBER: 38,414
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 418-3001
TELEPHONE: (512) 418-351
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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Pred. No. 9.8e-151;
0; Mismatches 28;
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Best Local Similarity 94.6%;
Matches 716; Conservative
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MEDIUM TYPE: Floppy disk
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; Sequence 3, Application US/09097199
; Patent No. 6218529
; GENERAL INFORMATION:
APPLICANT: Ah. Gang
APPLICANT: O'Hara, S. Mark
APPLICANT: Neltri, Robert
TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
TITLE OF INVENTION: PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                       61 AGAGATTGCTACAAAATCTTCTGAAGGGTCTCAATGGCTTCAGGCTAAGAAGAGATTTCTC
                                                                                                                                                                                                                                  CCTGTTATAAGCAGCAAGACAAATTAGCCATTTCACTCTCAAACTTCACTAATGATCACA
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                              1 ACAACGACACATTCAGGAGTTAAATATTTATCATCAAACATTGGATTTTTCCTTAACGCT
                                                                                                  1746 AGAGATTGCTACAAATCTTCTGAAGGGTCTCAATGGCTTCAGGCTAAGAAGAGATTTCTC
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2393 AGGAGGCTGAGGCGGAGAATTGCTTGAACCCGGAAGG 2429
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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2333 TACTAAAAACACAAAAATTAGCCGGGCGTGGTGGCACATGCCTGTAATCCCAGCTACTC 2392
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                                                                                                               721 AGGAGGCTGAGGCGGAGAATTGCTTGAACCCGGAAGG 757
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Pred. No. 6.2e-137;
1; Mismatches 4;
                                                                                                                                                                                            RESULT 7
2-09-949-016-119365/c
; Sequence 119365, Application US/09949016
; Patent No. 6812339
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98.8%;
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Best Local Similarity 98.87
Matches 596; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CRGANISM: Human
US-09-949-016-119365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 119365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.0%; Score 626.2; DB 3; Length 757; 94.6%; Pred. No. 9.8e-151; ive 0; Mismatches 28; Indels 13
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,199
FILING DATE:
CLASSIFICATION:
                                                                                                                                          PRICE APPLICATION DATA:

APPLICATION NUMBER: US 08/692,787
FILING DATE: 31-UL-1996
ATTORNEY AGENT INFORMATION:

NAME: Nakashima, Richard A.

REGISTRATION NUMBER: P-42,023
REFERENCE/DOCKET NUMBER: UROC:018
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 41-7577
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 757 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 94.6
Matches 716; Conservative
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 207012 543 121 484 181 424 241 364 301 304 361 244 421 184 481 541 64 122 GAAATATGAGGATATGCACAATATTATTCACATTTTACAGATCAGAAAATTGAGGCACAG 483 GAAATATGAGGGATATGCACAATATTTTTACAGATCAGAAAATTGAGGCACAG 243 GACCATGAAAGGTTCCTCAATGAAATGTTCCTCATTATCTTCAGAAGCCATATTATTATCAC 422 ATTGACTTTGCAGTTAACTCAGACCCTAGGTCTGGAATGCTGTCTTCTCTACTTATCCAA 482 AACTATACATCCACAGATCATATAAACTCTCAGCCCTGCTGCAAAGCCTTTCCAGAAAAA 2 ACCTTAAATATATCGAGGTGGCTAATTGATGTATAATAATTTACAAAATTATTCTTCTAT 62 IGCTACAGAGCTACAATTCAATTTACAGTAGGCCCACCATGAGGGCCTTCTTAAGGAACCA 542 IGCTACAGAGCTACAATTTACAGTTACAGTA-GTAAATATGAGGGGCCTTCTTAAGGAACCA 182 ATTAAGTAACTTCCCAAGGCTACCAGGCATTCTAGCTCCAGAAACTGTGCTCTTACCATT 423 ATTAAGTAACTICCCAAGGCTACCAGGCATTCTAGCTCCAGAAACTGTGCTCTTACCATT 303 CAYTGATTATTCCATAGAACAGTCACACCATGCAATTCTCACACCCTTGCAGACACACTT GACCATGAAAGGTTCCTCAATGAAATGTTCCTCATTATCTTCAGAAGCCATATTATTCAC CTGCTACAAGGTATTTCGAAAAAAAAAAGTAAAAAAAAAGAAGTCAAAAAGGCAACAGAGTT CATTGATTATTCCATAGAACAGTCACACCATGCAATTCTCACACCCTTGCAGACACACTT Gaps

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Sequence 119367, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
Patent No. 6812339

GENERAL INFORMATION:
PAPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FLIING DATE: 2000-10-20

PRIOR FLIING DATE: 2000-10-03

PRIOR FLIING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 119367

LENGTH: 601
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123 ACAGATCATATAAACTCTCAGCCCTGCTGCAAAGCCTTTCCAGAAAATAAAAATGGTTG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    601 ACTCCCTTCCACTTT-GTAATACCAGAACTCTAATTGGA-CACCCTGAAGCTTAGGACTA
                                        554 AAAAGGCAATTCTGCTACCAATGACTGTTTAAGCCCAGCCAAGTAACTGAACCATTCCAA
                                                               63 AAAAGGCAATTCTGCTACCAATGACTGTTTAAGCCCAGCCAAGTAACTGAAACTAAACCATTCCAA
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98.6%;
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Best Local Similarity 98.6
Matches 432; Conservative
                                                                                                                                                                                                                                                         US-09-949-016-119367/c
                                                                                                                          614 CTT 616
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US-09-949-016-119367
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                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: 06/241,755
RICOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FasteSEQ for Windows Version 4.0
LENGTH: 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              493
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                                        63 TAAAAATGGTTGAAAAGGCAATTCTGCTACCAATGACTGTTTAAGCCCAGCCCAAGTAAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       374 TICCICAAIGAAAIGIICCICAIIAICIICAGAAGCCAIAIIATICACAIIGACIIIGCA
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                                                                                                                                                                                                                                                       Sequence 119366, Application US/09949016
Patent No. 6812339
                                                                                                   502 GAA 604
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ORGANISM: Human
US-09-949-016-119366
                                                                                                                                              3 GAA
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Best Local S:
Matches 596
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Query Match
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                                                   FACULANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SSOFTMARE: FABLESQ for Windows Version 4.0
SSO ID NO 119364
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Patent No. 681239
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR PAPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-00
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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Best Local Similarity 98.1%; Pred. No. 1.7e-78;
Matches 368; Conservative 1; Mismatches 4; Indels 2
US-09-949-016-119364/c
; Sequence 119364, Application US/09949016
; Patent No. 6812339
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; ORGANISM: Human
US-09-949-016-119364
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US-09-949-016-16509
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Sequence 121999, Application US/09949016

| Sequence 121999, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VERTER, J. Craig et al.
| APPLICANT: VERTER, J. Craig et al.
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| FILE REFERENCE: CL001307
| CURRENT PILING DATE: 2000-04-14
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-10-03
| PRIOR APPLICATION NUMBER: 60/231,498
| PRIOR PILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SOFTWARE: FASESEQ for Windows Version 4.0
| SEQ ID NO 11999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 7.6%; Score 189.4; DB 4; Length 174639; Similarity 81.7%; Pred. No. 1.1e-37; 16; Conservative 0; Mismatches 46; Indels 9;
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 16509
LENGTH: 174639
                                                                                                                                                                                                                                                            FEATURE:

NAME/KEY: misc feature

LOCATION: (1)...(174639)

CTHER INFORMATION: n = A,T,C or G

US-09-949-016-16509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 81.7
Matches 246; Conservative
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US-09-949-016-121999
                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Human
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42396

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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,768
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-0-09-08
PRIOR PILING DATE: 2000-0-09-08
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Sequence 163069, Application US/09949016

Sequence 163069, Application US/09949016

Sequence 163080, Application US/09949016

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016
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                                      TGTAATCCCAGCTACTCAGGAGGCTGAGGC-GGAGAATTGCTTGAACCCGGAAGGTGGAG
      2442 CGGTGAGCTGAGATTGCACTATTGCACTCCAGCCTGGGCAACAGGAGTAAAACTCCCCCC
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84.5%; Pred. No. 1.1.
0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                           US-09-949-016-15165/c
; Sequence 15165, Application US/09949016
; Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 84.5
Matches 261; Conservative
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPERENCE: CLOO1307
CURRENT PILING DATE: 2000-04-14
CURRENT PILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 16308
LENGTH: 48691
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105 TIGITAGGAATGTCTAAGCAGGCCAGGCACGGTGGCTGACGCCTATAATCCCAGCACTTT 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature; LOCATION: (1).T.(48691); OTHER INFORMATION: n = A,T,C or GUS-09-949-016-16308
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FEATURE:
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US-09-949-016-16308
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                                                                                                                                                                                                                                                                                    Query Match
7.5%; Score 187.6; DB 4; Length 601;
Best Local Similarity 83.1%; Pred. No. 2.4e-38;
Matches 251; Conservative 1; Mismatches 40; Indels 10.
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 163069
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; ORGANISM: Human
US-09-949-016-163069
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12364.714 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
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| cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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                                                                                                                                                                                                                                                  September
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2506
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Maximum DB seq
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Š.

Description	Sequence 85, Appl Sequence 83, Appl Sequence 13, Appli Sequence 16, Appl Sequence 6897, Ap Sequence 251, App
ΠD	US-09-974-546-85 US-09-974-546-83 US-09-974-546-3 US-10-322-696-16 US-10-719-993-6897 US-09-860-670-251 US-10-227-646-251
DB	10 10 10 10 10 10 10 10 10
Query Match Length DB	2505 2087 2087 299598 129447 14417
Query Match	99.5 77.8 7.6 7.6 4.7
Score	2494 1950 626.2 190.6 189.4 186.4

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APPLICATION NUMBER: 09/097,199

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570-	-10-227	-10-027-632-1	-632-1	-632	-10-027-632-1	10-741-600	10-027-632-26658	10-027-632	US-10-956-157-7352	10-887-553	-157 - 211	10-153-668-43	10-027-632-11	10-027-632-1	10-027-632-1126	10-027-632	10-301-832	10-856-888	10-856-888-1	10-292-798-178	-161-	10-027-63	10-027-632-1	US-10-027-632-22469	10-027	10-723-860-200	9-188	10-723-860-13	-281-11	-09-918-995-238	10-087-192	10-331-053-6	-10-087-192-3	10-017-161-98	S-10-087-192-8	US-09-860-670-252	US-10-227-646-252
σ	11	13	13	17	11	21	13	17	21	21	21	14	13	13	11	17	19	20	20	17	15	13	17	13	17	50	22	20	19	10	13	19	13	15		σ	17
14426	14426	532	532	532	532	43623	450	450	9	1449	1449	1599	3079	3079	3079	3079	44348	9	106746	80	108317	585	585	723	723	110665	110665	227968	73723	463	89625	90614	71048	16156	91760	14426	14426
7.4	7.4	7.4	7.4	7.4	7.4		7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	•	•	7.3	٠			7.3	7.3	7.3	7.3	7.3	7.3	7.3	٠	7.3	7.3	7.3	•	7.3	٠	•	7.2
186.4	186.4	•	186.2	186.2	186.2		184.6	184.6	184.4	184.4	184.4	184.4	184.4	184.4	184.4	184.4	183.8	183.6	183.6	183.6	183.6	183.4	183.4	183.4	183.4	183.2	183.2	183.2	183	182.8	182.6	182.6	182.2	182	181.8	181.6	181.6
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ALIGNMENTS

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Sequence 85, Application US/09974546
Publication No. US20030050470A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Ralph, David
Veltri, Robert
Veltri, Robert
FITLE OF INVENTION: PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/974,546
FILING DATE: 10-Oct-2001
CLASSIFICATION: Unknown
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                  White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                        STREET: P.O. Box 4433 CITY: Houston
                                                                                                                                                                                                                                                                                                  ADDRESSEE: Arnold,
                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 77210
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                        STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
RESULT 1
US-09-974-546-85
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1020 1020 1080

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TCTGTCTCCATTAGTCAATAACTAAACTAACGAGCAATTAGTAAGCCATGTGCCAGAT
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                                                                                                                                                                                                                                                                                                             Length 2505
                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                          Query Match 99.5%; Score 2494; DB 10; Best Local Similarity 100.0%; Pred. No. 0; Matches 2505; Conservative 0; Mismatches 0;
         ATTORNEY/AGENT INFORMATION:
NAME: Nakashima, Richard A.
REGISTRATION NUMBER: P-42,023
REFERENCE/DOCKET NUMBER: UROC:018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 2505 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 99..503
SEQUENCE DESCRIPTION: SEQ ID NO: 0.9-974-546-85
 FILING DATE: 1998-06-12
                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                  FEATURE
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Copyright (c) 1993 - 2005 Compugen Ltd.
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7.9%; Score 198.8; DB 9; Length 700;

Query Match

HSM804005 BQ021987

AJ573255 AI031759 BU736145

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Gaps

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Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbert Strausberg, Ph.D.
Email: cgapbert Strausberg, Ph.D.
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NISC nb01f07.x1 COGENE 6E MAN Homo sapiens cDNA clone IMAGE:5795076
CB217256
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 586)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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//clone_lib="CGENE_GE MAN"
//note="Vector: pAMP1; cDNA primed using oligo-dT primer,
directionally cloned into UDG sites of pAMP1. Size
selected for insert sizes ranging from 0.2-2.0 kb.
                                                                                                                                                                                                                                                                                                                                                                                 2263 GGAGGT-----GGGTGGATCACCTGAGGTCGGGAGTTCGAGACCAGCCTGACCATG
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/tissue_trpe="mandible, pooled"
/dev_stage="embryo, 6 weeks postconception"
/lab_host="DH10B"
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                                                                                                                                                                              38;
                                                                                                       DB 8;
                                                                                                   Query Match 7.7%; Score 194.2; DB 8
Best Local Similarity 84.0%; Pred. No. 1.5e-25;
Matches 258; Conservative 0; Mismatches 38
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Seg primer: -21M13 forward primer (ABI)
Location/Qualifiers
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SOURCE
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Genomic survey sequence.
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                                                                                                                                                                                                                                                                                     363 GCCAAGGTGGGTGGATCACCTGAGGTCAGGAGTTCGAGACCAGCCTGACCAACATGG-AG 305
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                                                                                                                                                                       423 ACATTAAAAAACGCAGCCGGGCATGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAG 364
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Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieters@dejong.med.buffalo.edu). Clones may be purchased from
BACFAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 490)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2381 TCCCAGCTACTCAGGAGGCTGAGGC-GGAGAATTGCTTGAACCCGGAAGGTGGAGGTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 TCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATTGCTTGAACCCAGGAGGAGGCTGT
                                                                                                   2207 ATATAAAATACCCCGGCCAGGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGG--
                                                                                                                                                                                                                                          2265 ----AGGTGGGTGGATCACCTGAGGTCGGGAGTTCGAGACCAGCCTGACCAGCATGGTGG
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                                          11; Gaps
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Other GSSs: RPCI-11-195E6.TJ
Other GSSs: RPCI-11-195E6.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0200
Fax: 301 838 0208
87.5%; Pred. No. 2e-26;
tive 0; Mismatches 27; Indels
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|db_xref="GDB:7574597"
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                                   Matches 266; Conservative
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An,G., O'Hara,S.Mark., Ralph,D. and Veltri,R.
Biomarkers and targets for diagnosis, prognosis and I
prostate, breast and bladder cancer
Patent: US 6218529-A 83 17-APR-2001;
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/organism="unknown"
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-MODEL=frame+_p2n.model -DEV=xlh
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-MODEL=frame+_p2n.model -DEV=xlh
-D=/Command line parameters:
-D=/Comp2_1/USPPTO spool/19099974546/runat_07092005_174502_20945/app_query.fasta_1.654
-DB=Genbmbl -OPMT=fastap -SUFFXT=p2n.rg=
-UNITS=bits -GTART=1 -END=-1 -MATRIX=blosum62 -TTRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pto -NORM=ext -HEAPSIZE=50 -MINLEN-0 -MALTLEN=20000000
-USER=US09974546 @CGN 1 1 2647 @runat_07092005 174502_20945 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-USER=US0997454 @CGN 1 1 2647 @runat_07092005 174502_20945 -NCPU=6 -ICPU=3
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-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Copyright (c) 1993 - 2005 Compugen Ltd.
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LLPFCYKVFRKKEKVKRSQKATEFIDYSIEQSHHAILTPLQTHLTMKGSSMKCSSLSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Bases 1 to 2103) An. G. Maka, C.S., Luo, G., Bright, S.P., Cazares, L., Wright, G.L. Jr. and Veltri, R.W. Cloning and characterization of UROC28, a novel gene overexpressed in prostate, breast, and bladder cancers Cancer Res. 60 (24), 7014-7020 (2000)
                                                                  158
                                                                                                                                 218
                                                                                                                                                                                                   278
                                                                                                                                                                                                                                                                      338
                                                                                                                                                                                                                                                                                                                                        398
                                                                                                                                                                                                                                                                                                       LeuThrProLeuGlnThrHisLeuThrMetLysGlySerSerMetLysCysSerSerLeu 100
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                                                                                                                                                                                                                                                                                                                                                                                                         399 TCTTCAGAAGCCATATTATTCACATTGACTTTGCAGTTAACTCAGACCCTAGGTCTGGAA 458
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An.G. and Veltri.R.W.
Direct Submission
Submitted (23-SEP-1999) UroSciences, UroCor, Inc., 840 Research
Parkway, Oklahoma City, OK 73104, USA
1. cation/Qualifiers
                                                  99 ATGAGGCCTTCTTAAGGAACCAGAATATGAGGATATGCACAATATTATTCACATTTTA
                                                                                                21 GlnileArgLysLeuArgHisArgLeuSerAsnPheProArgLeuProGlyIleLeuAla
                                                                                                                                                                                         61 ArgSerGlnLysAlaThrGluPheIleAspTyrSerIleGluGlnSerHisAlaIle
                                                                                                                                                                                                                                                           279 AGAAGTCAAAAGGCAACAGAGTTCATTGATTATTCCATAGAACAGTCACACCATGCAATT
                                                                                                                                                                                                                                                                                                                                      339 crcacacccrrdcagacacacrrgaccargaaaggrrccrcaargaaargrrccrcarra
                                 MetArgAlaPheLeuArgAsnGlnLysTyrGluAspMetHisAsnIleIleHisIleLeu
                                                                                                                      159 CAGATCAGAAAATTGAGGCACAGATTAAGTAACTTCCCAAGGCTACCAGGCATTCTAGCT
                                                                                                                                                                    41 ProGluThrValLeuLeuProPheCysTyrLysValPheArgLysLysGluLysValLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF189270 2103 bp mRNA linear Homo sapiens UC28 protein (UC28) mRNA, complete cds. AF189270
                                                                                                                                                                                                                                                                                                                                                                                                                                                          type="prostate cancer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAG17118.1"
/db_xref="G1:10441604"
US-09-974-546C-86 (1-135) x AR146835 (1-2087)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product="UC28 protein"
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/gene="UC28"
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AUTHORS
TITLE
JOURNAL
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MEDLINE
PUBMED
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AF189270
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EMERGE STATES (TOTATES) Craniata, Vertebrata; Euteleostomi; Envaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 2496)
Strausberg, E.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N. K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubhn, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodersen, M., Rodrigues, S., Fahey, J., Helton, E., Ketteman, M., Madan, A., Kodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2496 bp mRNA linear PRI 23-JUN-2004 Homo sapiens prostate and breast cancer overexpressed 1, mRNA (cDNA BC069109
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135
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EAILFTLTLOLTQTLGLECCLLYLSKTIHPQII"
1961. .2103
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Matches:
Conservative:
Mismatches:
Indels:
                                                                          /note="alternative splicing"
2047. .2052
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694.00
100.00%
100.00%
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Best Local Similarity:
Query Match:
DB:
                             misc_feature
                                                                                                          polyA_signal
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455

PAT 08-AUG-2001

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1 (bases 1 to 2505)
An,G., O'Hara,S.Mark., Ralph,D. and Veltri,R.
Biomarkers and targets for diagnosis, prognosis and management of prostate, breast and bladder cancer
Patent: US 621829-A 85 17-APR-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339 CTCACACCCTTGCAGACACACTTGACCATGAAAGGTTCCTCAATGAAATGTTCCTCATTA
       396 TCTTCAGAAGCCATATTATTCACATTGACTTTGCAGTTAACTCAGACCCTAGGTCTGGAA
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                                          121 CysCysLeuLeuTyrLeuSerLysThr11eHisProGln11e116 135
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Mismatches:
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Matches:
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                                                                                                                                                 2505 bp
US 6218529.
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                                                                                                                                                                                                                                                                                                                                                                                                  1. .2505
/organism="unknown"
/mol_type="unassigned
                                                                                                                                                 AR146836
Sequence 85 from patent
AR146836
AR146836.1 GI:15110025
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Homo sapiens (human)
                                                                                                                                                                                                                                                                           Unclassified.
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Best Local Similarity:
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AUTHORS
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AF189269
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AR146836
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Location/Qualifiers
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.L., Skalski, U., Smallus, D.E.,
Schnorch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                  Direct Submission
Submitted (16-APR-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ArgSerGlnLysAlaThrGluPheIleAspTyrSerIleGluGlnSerHisHisAlaIle
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                                                                                                                                                                                                                                                                 NIH-MGC Project UKL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Anup Madan, University of Iowa
CDNA Library Preparation: Anup Madan, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Neurogenomics Research Lab,
200 B ENRB, University of Iowa, Iowa City, IA-52242
anup-madan@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                       Jessica Fahey, Tim Nelson, Jae Goon Yoon and Anup Madan
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
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Pred. No.:
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KEYWORDS
SOURCE
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2487. . 2492
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1 (bases 1 to 2512)
An, G. Ng, A.Y., Meka, C.S., Luo, G., Bright, S.P., Cazares, L., Wright, G.L. Jr. and Veltri, R.W.
Cloning and characterization of UROC28, a novel gene overexpressed in prostate, breast, and bladder cancers
Cancer Res. 60 (24), 7014-7020 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 ATGAGGCCTTCTTAAGGAACCAGAAATATGAGGATATGCACAATATTATTCACATTTTA 158
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An,G. and Veltri,R.W.
Direct Submission
Submitted (23-SEP-1999) UroSciences, UroCor, Inc., 840 Research
Parkway, Oklahoma City, OK 73104, USA
Location/Qualifiers
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Conservative:
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                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/RGP/Chre RPI-11M11 is from the library RPCI-1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                  HS171N11 129227 bp DNA linear PRI 04-MAR-2003
Human DNA sequence from clone RP1-171N11 on chromosome 6q23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 129227)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (04-MAR.2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 13, 1999 this sequence version replaced gi:4582115.
---------------- Genome Center
Center: Wellcome Trust Sanger Institute
129227
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Conservative:
Mismatches:
Indels:
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Contact: humquery@sanger.ac.uk
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                                                                                                                                                                                                                                                                  complete sequence.
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Pred. No.:
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MetArgAlaPheLeuArgAsnGlnLysTyrGluAspMetHisAsnIleIleHisIleLeu
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                                              NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                        4769: contig of 4769 bp in length
4869: gap of unknown length
11657: contig of 6788 bp in length
11757: gap of unknown length
28189: contig of 16432 bp in length
28289: gap of unknown length
53441: gap of unknown length
102327: contig of 285052 bp in length
102427: gap of unknown length
102427: gap of unknown length
182781: contig of 80354 bp in length
182781: contig of 80354 bp in length
186698: contig of 3817 bp in length.
Quality coverage: 5.84 in Q20 bases, agarose-fp Quality coverage: 5.57 in Q20 bases; sum-of-contigs
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/note="assembly_name:Contig12"
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                                                                30192 TCTTCAGAAGCCATATTATTCACATTGACTTTGCAGTTAACTCAGACCCTAGGTCTGGAA 30251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACUJ6236 186698 bp DNA linear HTG 01-SEP-2000
Homo sapiens chromosome 6 clone RP11-133015, WORKING DRAFT
SEQUENCE, 7 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (07-APR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Sep 1, 2000 this sequence version replaced gi:7523932.
                                                                                                                                                                                                                                                                                                                                                    LeuThrProLeuGlnThrHisLeuThrMetLysGlySerSerMetLysCysSerSerLeu 100
                                                                                                                                                                                                                                                                                                                                                                                                                        SerSerGluAlaIleLeuPheThrLeuThrLeuGlnLeuThrGlnThrLeuGlyLeuGlu 120
                                                                                                                                                                                                        41 ProGluThrValLeuLeuProPheCysTyrLysValPheArgLysLysGluLysValLys 60
                                                                                                                                          40
                                                                                                                                                                                                                                                                              61 ArgSerGlnLysAlaThrGluPheIleAspTyrSerIleGluGlnSerHisHisAlaIle 80
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 186698)
Waterston,R.H.
                                                                                                                                      21 GlnileArgLysLeuArgHisArgLeuSerAsnPheProArgLeuProGlyIleLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Washington University Genome Sequencing Center
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                               US-09-974-546C-86 (1-135) x HS171N11 (1-129227)
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Unpublished
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AC036236.2 GI:9958166
HTG: HTGS PHASE1; HTGS_DRAFT.
HOMO SADIEMS (human)
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Waterston, R.H.
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12 I (Dases I to 259920)
13 Maria, C., Allari, Alabrooks, S., Amin, A., Anguiano, D., Allari, C., Allari, M., Alabrooks, S., Amin, A., Anguiano, D., Allari, C., Allari, H., Alabrooks, S., Amin, A., Anguiano, D., Anguiano, D., Bandaranaike, D., Barber, M., Barasead, M., Benahmed, F., Bladdin, D., Bandaranaike, D., Barber, M., Barasead, M., Benahmed, F., Bladdin, D., Blari, C., Carel, S., Chan, M., Care, D., D'Souza, L., Cardara, V., Chare, D., Chavez, D., Chavez, D., Chavez, D., Chavez, D., Chavez, D., Chavez, D., Chavez, D., Chavez, D., Chavez, D., Chavez, D., Chavez, D., Chare, C., Chan, R., Chan, C., Chen, Z., Chan, D., Davila, M., Davis, C., Davez, D., Ding, Y., Chan, Dind, R., Dind, R., Dind, R., Dind, R., Dind, R., Dind, R., Dind, R., Dind, R., Dind, R., Dind, R., Dind, R., Dind, R., Dind, R., Dind, R., Dind, R., Dind, R., Dind, R., Dind, R., Dind, R., Care, C., Evans, C.A., Rallo, T., Fangon, M., Berandez, S., Finley, M., Fangon, R., Carder, R., Gartza, M., Gabrara, W., Gabrara, M., Gabrara, M., Gabrara, M., Gabrara, M., Gabrara, M., Gabrara, M., Gabrara, M., Gabrara, M., Gabrara, M., Gabrara, M., Gabrara, M., Gabrara, M., Gabrara, M., Gabrara, M., Gabrara, M., Gabrara, M., Gabrara, M., Gabrara, M., Havlak, P., Hawee, A., Handerson, M., Harlak, D., Havlak, P., Hawee, A., Handerson, M., Harlak, M., Jacob, L., Jang, H., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., 
                                                            159552 TCTTCAGAAGCCATATTATTCACATTGACTTTGCAGTTAACTCAGACCCTAGGTCTGGAA 159611
159432 AGAAGTCAAAAGGCAACAGAGTTCATTGATTATTCCATAGAACAGTCACACCATGCAATT 159491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accessed places. 259920 bp DNA linear HTG 10-MAY-2003 Rattus norvegicus clone CH230-18J15, WORKING DRAFT SEQUENCE, 2 unordered pieces.
                                                                                                                                                                                        SerSerGluAlaIleLeuPheThrLeuThrLeuGlnLeuThrGlnThrLeuGlyLeuGlu 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                             159612 TGCTGTCTTCTCTACTTATCCAAAACTATACATCCACAGATCATA 159656
                                                                                                                                                                                                                                                                                                                        121 CysCysLeuLeuTyrLeuSerLysThrIleHisProGlnIleIle 135
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AC096345.6 GI:30521870
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA.

On May 10, 2003 this sequence version replaced gi:24818617.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.uc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
                                                                                                                                                                                                                                                                                                                        Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (Dasses 1 to 259920) Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: Bstimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, Y., Zhao, S., Dunn, D., von Niederhausern, A., Waiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinscock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assembly program: 1 cucles 3.0;
Consensus quality: 240867 bases at least Q40
Consensus quality: 244203 bases at least Q20
Consensus quality: 245971 bases at least Q20
Estimated insert size: 252807; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 258395: contig of 258395 bp in length 258396 258495; gap of unknown length 258496 259920: contig of 1425 bp in length. Location/Qualifiers
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Center: Baylor College of Medicine

    .259920
    /organism="Rattus norvegicus"

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/note="wgs end_extension
clone_end:T7"
8054._.8862
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/note="clone_boundary
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                                                                                                                                                                                                                                                        Worley, K.C.
Direct Submission
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3098
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Homo sapiens isolate Berg 26 22q11.2 noncoding genomic sequence.
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2955 TTTATAATTICTCAAAAATCCTATGAGCCAGRIATGTAAATCTATATTITGCAGATACAG 3014
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                                                 11005839
2 (Dases 1 to 9833)
2 (Dases 1 to 9833)
Pamilo, P., Trexler, M., Patthy, L., Jorde, L.B., Yu, N. and Li, M.-H.
Direct Submission
Submitted (01-AUG-2000) Human Genetics Center, University of Texas
at Houston Health Science Center, 6901 Bertner Ave., Houston, TX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 LysLeuArgHisArgLeuSerAsnPheProArgLeuProGlyIleLeuAlaProGluThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 ValLeuLeuProPheCysTyrLysValPheArgLysLysGluLysValLysArgSerGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 LysAlaThrGluPhelleAspTyrSerIleGluGlnSerHisHisAlaIleLeuThrPro
on human chromosome 22
Proc. Natl. Acad. Sci. U.S.A. 97 (21), 11354-11358 (2000)
20481912
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                               1. .9833
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1. .9833
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34.10%
24.28%
13.69%
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Best Local Similarity:
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195470 TTTGAGGATGTGCAGGAGGACGATACTTTTCACAACTAAGGTTAGAAAGACATCATCTG 195411
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( basea 1 to 9833)

Zhao,Z., Jin,L., Fu,Y.-X., Ramsay,M., Jenkins,T., Leskinen,E., Pamilo,P., Trexler,M., Patthy,L., Jorde,L.B., Yu,N. and Li,W.-H. Worldwide DNA sequence variation in a 10-kilobase noncoding region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 AlalleLeuThrProLeuGlnThrHisLeuThrMetLysGlySerSerMetLysCysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 TyrGluAspMetHisAsnIleIleHisIleLeuGlnIleArgLysLeuArgHisArgLeu
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Homo sapiens isolate Japanese 18 22q11.2 noncoding genomic
sequence.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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           end_gequence.BH359975"
complement (248170. .249015)
clone="clone boundary
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site:EcoR1
end_sequence:BH360032"
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clone_end:Sp6"
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TTACAGAAGTGCTTAGCATATCTT 195075
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40.54%
25.68%
14.34%
site:EcoRI
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PRI 24-OCT-2000
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 9817)
Zhao,Z., Jin,L., Fu,Y.-X., Ramsay,M., Jenkins,T., Leskinen,E.,
Pamilo,P., Trexler,M., Patthy,L., Jorde,L.B., Yu,N. and Li,W.-H.
Worldwide DNA sequence variation in a 10-kilobase noncoding region
on human chromosome 22
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                   3279 AAAATGGAACCACATGGTCTGTTCCTGAATTCTCCAACAGATCCCTTTGGTCCCAACCTC 3338
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Din,L., Fu,Y.-X., Ramsay,M., Jenkins,T., Leskinen,E.,
Pamilo,P., Trexler,M., Patthy,L., Jorde,L.B., Yu,N. and Li,W.-H.
Direct Submission
Submitted (01-MUG-2000) Human Genetics Center, University of Texas at Houston Health Science Center, 6901 Bertner Ave., Houston, TX
77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 LeuGlnThrHisLeuThrMetLysGlySerSerMetLysCysSerSerLeuSerSerGlu 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 ValLeuLeuProPheCysTyrLysValPheArgLysLysGluLysValLysArgSerGln 63
                                                                                                                                                                    AF291631 9817 bp DNA linear PRI 24-OCT-200
Homo sapiens isolate South African MeJe 22q11.2 noncoding genomic
sequence.
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42
17
38
76
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                                                             120 GluCysCysLeuLeuTyrLeuSerLysThrIleHisPro
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/mol_type="genomic_DNA"
/isolate="South African MeJe"
/db_xref="txxon:9606"
/mosome="22"
/map="22q11.2"
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/organism="Homo sapiens"
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/note="noncoding region"
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                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
[1 (bases 1 to 9432)
[2 Aao, Z., Jin, L., Fu, Y.-X., Ramsay, M., Jenkins, T., Leskinen, E., Pamilo, P., Trexler, M., Patthy, L., Jorde, L.B., Yu, N. and Li, W.-H. Worldwide DNA sequence variation in a 10-kilobase noncoding region
                                                                                                                                                                                                                                                                                                                           Zhao, Z., Jin, L., Fu, Y.-X., Ramsay, M., Jenkins, T., Leskinen, E., Pamilo, P., Trexler, M., Patthy, L., Jorde, L.B., Yu, N. and Li, W.-H. Direct Submission
Submitted (01-AUG-2000) Human Genetics Center, University of Texas at Houston Health Science Center, 6901 Bertner Ave., Houston, TX 77030, USA
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                                                                                                                                                                                                                           on human chromosome 22
Proc. Natl. Acad. Sci. U.S.A. 97 (21), 11354-11358 (2000)
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Matches:
Conservative:
Mismatches:
Indels:
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Organism="Homo sapiens"

/mol type="genomic DNA"

/isolate="Berg 26"

/db_xref="taxon:9606"

/chromosome="22"

/map="22q11.2"

1. .9432

/note="noncoding region"
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AF291608.1 GI:10953210
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                                                           sapiens (human)
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Best Local Similarity:
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Direct Submission
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AF291588 9833 bp DNA linear PRI 24-OCT-2000
Homo sapiens isolate Chinese 2 22q11.2 noncoding genomic sequence.
AF291588
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Jaho, Z., Jih, L., Fu,Y.-X., Ramsay,M., Jenkins,T., Leskinen,E.,
Pamilo,P., Trexler,M., Patthy,L., Jorde,L.B., Yu,N. and Li,W.-H.
Worldwide DNA sequence variation in a 10-kilobase noncoding region
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Proc. Natl. Acad. Sci. U.S.A. 97 (21), 11354-11358 (2000)
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Matches:
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3051 GTAGATCTGGGATTT----- 3065
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Zhao, Z., Jin, L., Fu, Y.-X., Ramsay, M., Jenkins, T., Leskinen, E., Pamilo, P., Trexler, M., Patthy, L., Jorde, L.B., Yu, N. and Li, W.-H. Direct Submission
Submitted (01-AUG-2000) Human Genetics Center, University of Texas at Houston Health Science Center, 6901 Bertner Ave., Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 LeuGlnThrHisLeuThrMetLysGlySerSerMetLysCysSerSerLeuSerSerGlu 103
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1. .9833
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Aax13160 Enterococ
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Ab102615 Drosophil
Ab10770 Drosophil
Ab107868 Drosophil
Adf50278 Human PFM
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/product= "Prostate cancer marker protein"
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ADN47960 09
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96US-0013611P.
96US-00692787.
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31-JUL-1996;
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Aas04583 Prostate
Aas04001 Biomarker
Aaz87584 Prostate
Adt45647 Bacterial
                                                                                  9; Search time 309 Seconds (without alignments) 2586.295 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1 MRAFLRNQKYEDMHNIHIL......TLGLECCLLYLSKTIHPQII 135
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Copyright (c) 1993 - 2005 Compugen Ltd.

    nucleic search, using frame_plus_p2n model

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                                                                                               New nucleic acids as biomarkers and targets useful for detecting, diagnosing, prognosing, and in developing treatments for prostate, breast and bladder cancer.
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Mismatches:
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                                      O'hara SM, Ralph D, Veltri R;
                                                                                                                                                     Claim 2; Col 117-121; 78pp; English.
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                                                             WPI; 2001-289849/30.
P-PSDB; AAU02174.
            (UROC-) UROCOR INC
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Best Local Similarity:
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TGCTGTCTTCTCTACTTATCCAAAACTATACATCCACAGATCATA

459

AAZ87583 standard; DNA; 2088 BP

AAZ87583

RESULT 2
AAZ87583
ID AAZ8
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AC AAZ8

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bladder cancer. The markers are indicators of majorant transformation of prostate, breast and bladder tissues and are diagnostic of the potential for metastatic spread of malignant prostate tumours. The mostate acid can also be used as targets for therapeutic intervention in prostate cancer, benign prostatic hyperplasia (BPH) bladder cancer or breast cancer. The markers may be used to design specific probes and primers, for the rapid malysis of prostate, bladder or breast bloppy samples. The probes and primers may also be used for in situ hybridization or in situ PCR detection and diagnosis. They may also be used to identify and isolate the polypeptide products of the markers can be used to treat prostate cancer. The polypeptide products of the markers can be used to treat prostate cancer, bladder cancer or breast cancer. The encoded proteins may be used to detect antibodies. The proteins and antibodies can be used in immunodetection methods for detecting or quantifying the cancers, and for clinical diagnosis of these cancers. The antibodies may also be used for
                                                                                                            Nucleic acid marker, biomarker, tumour, prostate cancer, bladder cancer, benign prostatic hyperplasia, BPH, breast cancer, human, immunodetection, diagnosis, PCR primer, 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention provides nucleic acid markers of prostate, breast and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2088 BP; 740 A; 406 C; 337 G; 604 T; 0 U; 1 Other;
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                                                    Prostate disease marker UC Band #28
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P-PSDB; AAY59295.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acids as biomarkers and targets useful for detecting, diagnosing, prognosing, and in developing treatments for prostate, breast and bladder cancer.
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CTCACACCCTTGCAGACACACATGAAAGGTTCCTCAATGAAATGTTCCTCATTA
                                                                                                        399 TCTTCAGAAGCCATATTATTCACATTGACTTTGCAGTTAACTCAGACCCTAGGTCTGGAA
                                            LeuThrProLeuGlnThrHisLeuThrMetLysGlySerSerMetLysCysSerSerLeu
                                                                                            SerSerGluAlaIleLeuPheThrLeuThrLeuGlnLeuThrGlnThrLeuGlyLeuGlu
                                                                                                                                                                                                                                                                                Biomarker UC band 28 #3, used in diagnosis and prognosis of cancer.
                                                                                                                                                                                                                                                                                                      Prostate; breast, bladder; cancer; biomarker; probe; diagnostic; benign prostatic hyperplasia; BPH; therapeutic; human; ss.
                                                                                                                                                     TGCTGTCTTCTCTACTTATCCAAAACTATACATCCACAGATCATA 503
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96US-0013611P.
96US-00692787.
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                                                                                                                                                                                                                                                         (first entry)
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P-PSDB; AAU02175.
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11-JAN-1996;
31-JUL-1996;
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Mismatches:
Indels:
  Length:
Matches:
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                                           Percent Similarity:
Best Local Similarity:
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The invention provides nucleic acid markers of prostate, breast and bladder cancer. The markers are indicators of malignant transformation of prostate, breast and bladder tissues and are diagnostic of the potential for metastatic spread of malignant prostate tumours. The nucleic acid can also be used as targets for therapeutic intervention in prostate cancer, benign prostatic hyperplasia (BPH), bladder cancer or breast cancer. The markers may be used to design specific probes and primers, for the rapid primers may be used to design specific probes and primers, for the rapid primers may also be used for in situ hybridization or in situ PCR detection and diagnosis. They may also be used to identify and isolate till length gene sequences form various DNA libraries. Antibodies against the polypeptide products of the markers can be used to treat prostate cancer, bladder cancer or breast cancer. The encoded proteins may be used to detect antibodies. The proteins and antibodies can be used in immunodetection methods for detecting or quantifying the cancers, and for climical diagnosis of these cancers. The encoded proteins and for climical diagnosis of these cancers. The encoded proteins
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                  Claim 1; Page 184-186; 191pp; English.
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The invention relates to a recombinant DNA construct comprising a prowoter functional in a plant cell, where the promoter is positioned to prowoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypoptide from a comprising the recombinant DNA construct and a method of producing a transformed plant excembinant DNA construct and of producing a transformed plant cauch as maize or sopbean. The method of producing a transformed plant cauch as maize or sopbean. The method of producing a transformed plant cauch and proved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties.

The recombinant DNA construct is useful for improving plant properties.

The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, colerance to hearbidides, extreme osmotic conditions or pathogens or peters, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased resistance to plant disease, better growth rate by modification of protein yield and/or content, improved yield by modification of erobohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved plants production or improved galactomannan production. This sequence represents a bacterial polynucleotide used in the scope of the invention. Note: The sequence data for this patent did form part of the printed specification but was obtained in electronic format from HRPD, at sandata users.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
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61 ATGCACAACTTA-----GCCATAAAGCTGAGAAAAGAGGGGGAAGAGGAATAGTC 114
pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polynucleotide; gene; ss.
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SLATER S C.
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                                                                                                  New recombinant DNA construct comprising a promoter positioned to provide
                   115 ACAAACAACAGGCCCACGGGAAAGGAAGAAGAGCTTAAGAGATATGGAATAGAGCTCATA 174
                                                                                                                                                                             93 SerSerMet---LysCysSerSerLeuSerSerGluAlalleLeuPheThrLeuThrLeu 111
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                                                                                                                                 73 IleGluGlnSerHisHisAlaIleLeuThrProLeuGlnThrHisLeuThrMetLysGly 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a
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                                                                                     54 ArglyslyslulysvallysArgSerGlnLysAlaThrGluPheile---AspTyrSer
                                                                 -----TTTTAGATGTA
                                        34 ArgLeuProGlyIleLeuAlaProGluThrValLeuLeuProPheCysTyrLysValPhe
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transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties.

The recombinant DNA construct is useful for improving plant properties.

CC polynucleotide or polypeptide is useful for producing plants with improved plant properties, e.g. improved conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of content, improved plant prower seed oil or protein yield and/or content, improved plant growth and development under at least on stress production. This sequence represents a bacterial polymucleotide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic content from USPTO at sequence.
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70 ATGCACAACTTA-----GCCATAAAGCTGAGAAAAGAGGGGATGAAGTGGGAATAGTC 123
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pharmaceutical; gene; ds.
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04-JUN-1
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                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABIJ1676-ABIJ0511), expressed DNA sequences (ABIJ1675) and the encoded proteins (ABBS7197). ABBS72072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1449 CATAGGCAGCCCATCACA-----TCCACATCGCATCAAAGAACGAAAAGAAAGCA 1499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerSerLeuSerSerGluAlaIleLeuPheThrLeuThrLeuGlnLeuThrGlnThrLeu 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 IleLeuAlaProGluThrValLeuLeuProPheCysTyrLysValPheArgLysLysGlu 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 HislleLeuGlnIleArgLysLeuArgHisArgLeuSerAsnPheProArgLeuProGly 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 LysValLysArgSerGlnLysAlaThrGluPheileAspTyrSerIleGluGlnSerHis 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 HisAlaileLeuThrProLeuGlnThrHisLeuThrMetLysGlySerSerMetLysCys 97
                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                            Sequence 4019 BP; 1158 A; 966 C; 927 G; 968 T; 0 U; 0 Other;
                                                                                                                                                                                                                     Claim 1; SEQ ID NO 34867; 21pp + Sequence Listing; English.
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                                                             23-MAR-2001; 2001WO-US009231
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11-JUL-2000; 2000US-00614150.
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89.50
39.84%
27.34%
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Drosophila melanogaster
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Best Local Similarity:
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Pred. No.:
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X Arabidopsis thaliana DNA fragment SEQ ID NO: 21658.

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X Arabidopsis thaliana DNA fragment SEQ ID NO: 21658.

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18 - JUN - 1999 18 - JUN - 1999 18 - JUN - 1999 18 - JUN - 1999 18 - JUN - 1999 18 - JUN - 1999 22 - JUN - 1999 23 - JUN - 1999 24 - JUN - 1999 25 - JUN - 1999 26 - JUN - 1999 27 - JUN - 1999 28 - JUN - 1999 29 - JUN - 1999	11-JUL-1999 20-JUL-1999 80-JUL-1999	22

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US-09-974-546C-86 (1-135) x AAC38626 (1-532)

30 SerAsnPheProArgLeuProGlylleLeuAlaProGluThrValLeuLeuProPheCys 49

8 8 8

G; 41031 T; 0 U; 0 Other;

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64001 of the PLCG1 gene (reference sequence GI 11345540) causing an amino acid charge from Threonine to Isoleucine at position 813 of the protein. This sequence represents the region of the PLCG1 gene with the T form of the polymorphism. The methods, agents and apparatus is used for diagnosing and prognosing vascular diseases e.g. atherosclerosis, coronary artery disease (especially), myocardial infarction (especially), isohemia, stroke, peripheral vascular diseases, venous thromboembolism and pulmonary embolism
                                                                                                                                                                                                                        Sequence 146547 BP; 39552 A; 32625 C; 33339
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97US-0046655P.
97US-0066009P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diagnosing and prognosing vascular disease, e.g. coronary artery disease and myocardial infarction, based on the detection of polymorphisms in the phospholipase C gamma 1 and plasminogen activator inhibitor type 2 genes and polypeptides.
                                                                                                        218
                                                                                                                                                                                                                                                                                                                       158
                                ---TGT 338
                                                                                                                                                                                                                                                                                                                                                                 SerLeu-----SerSerGluAlaIleLeuPheThrLeuThrLeuGlnLeuThrGln 115
                                                                             68
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                                                                                                                                                                                                                                                                                                217 CAACCCGTGAACCCAGCCATCATCTTCTGACCTCCATTTCCCCAGTACCTCGTGTCTC
                                                                                                                                                                                                                                                                     -----ProLeuGlnThrHisLeuThrMetLysGlySerSerMetLysCysSer
                                                                                                                                                                         -----IleAspTyrSerIleGluGlnSerHisHisAla-----IleLeuThr---
                                                                                                                                                                                                                      277 GITITIGICATAACITICAGCATCICACITGCAAACGCIGCAGAIGIGCIGACCGGC
                                                                          50 TyrLysValPheArgLysLysGluLysValLysArgSerGlnLysAlaThrGluPhe---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human; single nucleotide polymorphism; SNP; phospholipase C gamma 1; PLCG1; gene; vascular disease; plasminogen activator inhibitor type 2 PAI-2; diagnosis; atheroaclerosis; coronary artery disease; ischemia; myocardial infarction; stroke; thromboembolism; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 ThrieuGlyLeuGluCysCys-----LeuieuTyrLeuSer 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 TCTCTTGCTACAGTGTTGTTCTGCGCTGATTCTCTGCTTATCA 71
  385 TATAACTTACCCAATCTAGTTTTGGCTTTGGCTTCCACGGAACA---
                                                                                                                                                                                                                                                                                                                                                                                               Human phospholipase C gamma 1 polymorphism G329ul.
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replace(64001,c)
/*tag= a
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2001US-0327488P.
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05-OCT-2001;
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variation
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29020 ATTATCCCCATTTTCCAGATGAAAAACTGAGGCACAGAGCTAAAAAGGCAGGATTCAAAC 28961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus facetalis genome. AAX12938 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus facetalis genome with commercial importance. The products can be used to detect the presence of Enterococcus facetalis in samples. They can also be used for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus infection.
                                                                                                                                                                  IlelleHisIleLeuGlnIleArgLysLeuArgHisArgLeuSerAsnPheProArgLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
                                                                                                                                                                                                                                                                  CCAGGTAGTCTGGCCCCAGAGTCAGTG-----TTTTGCTTC 28922
                                                                                                                                                                                                                                          ProGlyIleLeuAlaProGluThrValLeuLeuProPheCysTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterococcus faecalis genome contig SEQ ID NO:223.
Length:
Matches:
Conservative:
Mismatches:
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                                                                          Indels:
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ID ABD3;
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                                                                                                                                                                                                                                                                             2452
                                                                                                                                                                                                                                                                                                                                                           Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nuclectide sequences can be used in vaccines to prevent or attenuate an Enterococcal infection
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                                                                                                                                                                                                             -----MetHisAsnIleIle----- 17
                                                                                                                                                                                                                                                        -------HisIleLeuGlnIleArgLysLeuArgHisArgLeuSerAsnPhe 32
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                                                                                                                                                                                                                                                                                                                                                                                        73 IleGluGlnSerHisHisAlaIleLeuThrProLeuGlnThrHisLeuThrMetLysGly
                                                                                                                                                                                                                                                                    ProArgLeuProGlyIleLeuAlaProGluThrValLeuLeuProPheCysTyrLysVal
                                                                                                                                                                                                                                                                                                                                             PheArgLysLysGluLysValLysArgSerGlnLysAlaThrGluPheIleAspTyrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                   93 SerSerMetLysCysSerSerLeuSerSerGluAlaIleLeuPheThrLeuThr----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 ---LeuGlnLeuThrGlnThrLeuGlyLeuGluCysCysLeuLeuTyrLeuSer 127
                                                                           Sequence 24601 BP; 8032 A; 4435 C; 5259 G; 6859 T; 0 U; 16 Other;
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Indels:
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Best Local Similarity:
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                                                                                                Alignment Scores:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a new computer readable medium with an diagnose the presence of E. faecalis in a sample or determining the presence of a specific microbe in a sample. The invention is useful to presence of a specific microbe in a sample. The invention is also useful for modulating the growth or pathogenicity of E. faecalis, in a vaccine to confer resistance to Enterococcal infection, for commercial, therapeutic and industrial purposes, and for fermenting a particular sugar source or to produce a particular metabolite. The invention is useful for detecting diseases related to Enterococcus infections in animals, and for detecting E. faecalis using biochip technology. The present nucleic acid sequence represents an Enterococcus faecalis contig DNA sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110
                                                                                                                                                                                                                                     Computer readable medium having recorded on it a Enterococcus faecalis nucleotide sequence useful for detecting diseases related to Enterococcus
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Matches:
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KUNSCH C P
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BARASH S.
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Conservative: Mismatches:

81.50 42.86% 29.37%

Best Local Similarity:

Percent Similarity:

Indels:

11.74%

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The invention relates to an isolated mucleic acid comprising at least 10 in the invention relates to an isolated mucleic acids encode cancer associated proteins. Also included are an expression vector comprising the isolated nucleic acid cited above, a host cell comprising the above ceremblant nucleic acid cited above, a host cell comprising the above ceremblant nucleic acid cited above, a host cell comprising the above ceremblant nucleic acid cited above, a microarray for detecting cemprising at least 10 contiguous nucleotides of any of the above comprising trame of a CA sequence selected from any of the above comprising frame of a CA sequence selected from any of the 35 complement), an isolated antibody, (or its antigen binding fragment) that binds to the above polypebtide, a hybridoma that produces the above monoclonal antibody, a pharmaceutical composition comprising the above mancolonal antibody, a pharmaceutical composition comprising the above mancolonal antibody, a pharmaceutical composition comprising the above methody and a pharmaceutical composition comprising the above methody and a pharmaceutical composition of cells in an antibody and a pharmaceutical composition comprising the above methody and a pharmaceutical composition and cells in an individual, a method for inhibiting growth of cancer cells in an individual, a method for delivering a therapeutic agent to cancer cells in an individual, an electronic library comprising the above polymeticancer activity or for a bloactive agent capable of modulating the activity of a CA protein (CAP), methods for inhibiting the expression of for anticancer activity or for a bloactive agent capable of modulating cancer associated with expression of a polypeptide in a test cell sample. These may also be used in screening for agents that modulate cancer. The present sequence is a mouse CAP generic data for this parent din or form part of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated cancer-associated polynucleotides and polypeptides useful for diagnosing, preventing or treating cancers, especially lymphoma and leukemia, or in screening for agents that modulate cancer.
                                                                                                                                 Mouse, ds, cancer-associated protein, gene, cytostatic, cancer, leukaemia, lymphoma, CAP.
                                                                                           Mouse cancer-associated genomic DNA MD13-011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Morris DW, Morris DW, Malandro MS,
                                                                                                                                                                                                                                                                                                                                                                                                              14-WAR-2003; 2003US-00388838.
15-APR-2003; 2003US-00417375.
13-JUN-2003; 2003US-00461862.
15-EEP-2003; 2003US-0066431.
15-DEC-2003; 2003US-00737318.
                                                                                                                                                                                                                                                                                                                                             17-FEB-2004; 2004WO-US004730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAGR-) SAGRES DISCOVERY INC
                                             (first entry)
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                                                                                                                                                                                                         Mus musculus,
                                           18-NOV-2004
ABD32622;
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Length:

6.32e+03

Alignment Scores: Pred. No.:

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9988 CTACATGCACTGCTAAATGGTGATGTCAGATTCGGTTTTACTAACTTCTCCAAA---- 9935
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                                                                                                                                                                                                                                               17 IleHisIleLeuGlnIleArgLysLeuArgHisArgLeuSerAsnPheProArgLeuPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 GluLysValLysArgSerGlnLysAlaThrGluPheIleAspTyrSerIleGluGlnSer
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37
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333
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9724 CATCCCTCCCAAGTCATC 9707
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11-JAN-2000; 2000US-00480902.
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MATHIALAGAN N
TAO N.
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of ADN47591 from base 900001 (Thermococcus kodakaraensis KOD1
21 fragments LOCUS ADN47591 Accession Adn47591
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Mismatches:
Indels:
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Matches:
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Continuation (10 of 21) of A
WP Sequence split into 21 fr
WP ADM47591_01
WP ADM47591_01
WP ADM47591_03
WP ADM47591_03
WP ADM47591_05
WP ADM47591_06
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WP ADM47591_06
WP ADM47591_06
WP ADM47591_07
WP ADM47591_07
WP ADM47591_08
WP ADM47591_08
WP ADM47591_08
WP ADM47591_10
WP ADM47591_10
WP ADM47591_11
110
WP ADM47591_11
110
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Query Match:
ADN46845 08
ADN46845 08
ADN46845 08
ADN46845 11
ADN46845 11
ADN46845 12
ADN46845 13
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ADN46845 13
ADN46845 13
ADN46845 14
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ADN46845_20
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LOCUS ADN46845 Accession Adn46845
                             The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically Mybridise to a second nucleic acid molecule comprising any of 1512 nuclectide sequences.

(a) appearing as ABX34836-ABX49947, or complements of them. Also included are idlined to a promoter and a 3' non-translated sequence that cardid linked to a promoter and a 3' non-translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement cell or complementary nucleic acid sequences or its complement cell or fissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) of tissue, where hybridisation between the marker nucleic acid, and the complementary nucleic acid permits the detection of the molecule; and (b) of effecting the level or pattern of the complementary nucleic acid sequence complementary nucleic acid permits the detection of the molecule. The LMFD nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for the complementary nucleic acid is used for the section of the molecule. The LMFD nucleic acid is used for the section of the molecule. The LMFD nucleic acid is used for the section of the molecule for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the selectronic format from the uspecification but was obtained in province LMFD EST (expressed sequence tag) nucleic acids. Note: The present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 AAGATAAGACACCAGATTCTCAAACTGCCAACTAGTCGTCTGCCCAGTAGCTGACGACGG 155
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Matches:
Conservative:
Mismatches:
Indels:
    Claim 2; SEQ ID NO 9738; 245pp; English.
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Continuation (12 of 21)
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ADN46845 00
ADN46845 01
ADN46845 02
ADN46845 03
ADN46845 04
ADN46845 04
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20895 AAAGTCCCGGGTGTCATCAGTCCG---GTGCTCGGGATAAACATAACCTAC----- 20942
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                                                                                                                                                                                                                                                                                                                     54 ArglyslysGlulysVallysArgSerGlnLysAlaThrGluPhe---IleAspTyrSer 72
                                                                                                                                                                                                                                                                           34 ArgleuProglyIleLeuAlaProGluThrValLeuLeuProPheCysTyrLysValPhe 53
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Search completed: September 9, 2005, 13:25:08 Job time : 388 secs

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73 IleGluGlnSerHisHisAlaIleLeuThrProLeuGlnThrHisLeuThrMetLysGly 92

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ઠે g ò Sequence 15729, A Sequence 5, Appli Sequence 14, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 125, Appli Sequence 12551, A Sequence 12551, A Sequence 17108, A Sequence 1759, A Sequence 17254, A Sequence 17254, A Sequence 17254, A Sequence 16739, A Sequence 16739, A Sequence 16739, A Sequence 16739, A Sequence 16739, A Sequence 16278, A Sequenc

Sequence:

Run on:

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09:59:42 2005
Sep 12
 Mon
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US-09-097-199-83
; Sequence 83. Application US/09097199
; Patent No. 6218529
; GENERAL INFORMATION:
APPLICANT: An. Gang
APPLICANT: O'Hara, S. Mark
APPLICANT: Veltri, Robert
; TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
TITLE OF INVENTION: PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,199
US-09-949-016-15729

US-08-573-080A-99

US-08-675-566-14

US-08-675-566-14

US-08-675-566-13

US-08-675-566-21

US-08-675-566-21

US-09-970-077-1826

US-09-949-016-12551

US-09-949-016-12551

US-09-949-016-12412

US-09-949-016-12412

US-09-949-016-12594

US-09-949-016-17554

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US-09-949-016-17554

US-09-949-016-12594

US-09-949-016-12594

US-09-949-016-12594

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US-09-949-016-157153
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US-09-949-016-16210
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
11LING DATE: 31-ULL-1996
ATTORNEY/AGENT INFORMATION:
NAME: NAKABIMA, RICHARD A.
REGISTRATION NUMBER: P-42,023
REFERENCE/DOCKET NUMBER: UROC:018
TELECOMMUNICATION INFORMATION:
                                                                                                                                              761
96878
462589
476044
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42672
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19008
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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-Q-/cgn2_1/USPTO_epool/US09974546/runat_07092005_174503_21006/app_query.fasta_1.654
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-DB=issued_Patents_NA -QFPMT=fastap_-SUFFIX=p2n.rmi -MINEATCH=0.1 -LOOPCL=0
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-LIST=45 -DOCALIGN=210 -NORM=ext -HRAPSIZE=500 -MINIEN=0 -ALIGN=15
-USPR=US09974546 @CGN 1 1 77 @runat_07092005 174503 21006 -NCPU=6 -ICPU=3
-NO WAAP -LARGEQUERY -NEG_SCORSE=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -TRHEADS=1 -XGAPO=10 -KGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 3311, Ap
Sequence 13053, A
Sequence 11936,
Sequence 119366,
Sequence 119364,
Sequence 21, App
Sequence 53, Appl
Sequence 53, Appl
                                                                                                                                 (without alignments)
2113.850 Million cell updates/sec
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                OM protein - nucleic search, using frame_plus_p2n model
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US-09-097-199-85
US-09-949-016-1311
US-09-949-016-15053
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US-09-949-016-119366
US-09-949-016-119364
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US-09-186-188B-53
US-09-265-585C-53
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                                                                                                                                                                                                                                                                                                                                                   1202784 seqs, 818138359 residues
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                                                                                                               September 9, 2005, 13:12:05
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Maximum DB seq length: 200000000
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Patent No. 6218529
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: O'Hara, S. Mark
APPLICANT: Ralph, David
APPLICANT: Veltri, Robert
TITLE OF INVENTION: PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSE: ARROIG, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CysCysLeuLeuTyrLeuSerLysThrIleHisProGlnIle11e 135
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                           Gaps:
TELEFAX: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 2087 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
FATURE:
NAVIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                     1.65e-85
694.00
100.00%
100.00%
                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: 99..503
US-09-097-199-83
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                         Alignment Scores:
Pred. No.:
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Sequence 3311, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISSASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 GlnIleArgLysLeuArgHisArgLeuSerAsnPheProArgLeuProGlyIleLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 CysCysLeuLeuTyrLeuSerLysThrIleHisProGlnIleIle 135
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                      PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                 CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,787
FILING DATE: 31-JUL-1996
ATTORNEY, AGENT INFORMATION:
NAME: NAKSSHIMA, RICHARD A.
REGISTRATION NUMBER: P-42,023
REFERENCE/DOCKET NUMBER: URCC:018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTER.STICS:
LENGTH: 2505 base pairs
TENGRATH: 2505 base pairs
                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,199
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.21e-85
694.00
100.00%
100.00%
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-09-949-016-3311
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LOCATION:
                        SOFTWARE:
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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00; Search time 408.5 Seconds (without alignments) 2170.324 Million cell updates/sec
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OM protein - nucleic search, using frame_plus_p2n model
                                          9, 2005, 14:46:00
                                                                                                                       US-09-974-546C-86
                                          September
                                                                                                                       Title:
Perfect score:
                                                                                                                                                                Sequence:
                                        Run on:
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7351250 seqs, 3283620254 residues 0.5 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext Searched:

BLOSUM62

Scoring table:

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

MODEL=frame+ planning to the planning of the planning of the planning plann

Published_Applications_NA:* Database :

"Ggn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

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(Ggn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

(Ggn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

(Ggn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

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(Ggn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

(Ggn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

(Ggn2_6/ptodata/2/pubpna/US10B_PUBCO /ptodata/2/pubpna/US11A PUBCOMB.seq: /ptodata/2/pubpna/US11 NEW PUB.seq:* /ptodata/2/pubpna/US60_NEW_PUB.seq:* ptodata/2/pubpna/US10 NEW PUB. seq: Cgn2_6/ Cgn2_6/ Cgn2_6/ Cgn2_6/ Cgn2_6/ Cgn2_6/ Cgn2_6/ Cgn2_6/ Cgn2_6/ Pred. No. is the number of results predicted by chance to have

/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

cription	Sequence 83,	Sequence	Sequence 440	Sequence 250	Sequence 318	Sequence 43:	Sequence 223	Seguence	Sequence	Seguence	4 Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	7 Sequence	Sequence	Sequence	Sequence 99, A	Sequence 744	Sequence 54224	1 Sequence 269701 1 Sequence 269701	o Sequence 133030	0 Sequence 133030 Sequence 15166	Sequence 5 Sequence	Sequence 13943	Sequence 10443,	Sequence	Sequence 8467	Sequence 84669	Sequence 1	1 Sequence 223621	5-10-424-599-5755 Sequence 5755, Ap 3-10-425-115-139430 Sequence 139430,	NTS) TARGETS FOR DIAGNOSIS, MANAGEMENT OF PROSTATE DISEASE	
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& Query Match	.00	100.0	13.0	13.0	12.5	12.0	11 8	11.7	11.7	11.7	11.7	11.6	11.6	11.6	11.6	11.6	11.6	11.5	11.5	11.5	11.5	11.5	11.4	11.4	11.4	11.4	11.4	11.3	11.3	11.3	11.3	11.2	11.2	11.2		,	6-83 3, Applica	INFORMATION:	: TANA.		OF INV	OF SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerSerGluAlaIleLeuPheThrLeuThrLeuGlnLeuThrGlnThrLeuGlyLeuGlu 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279 AGAAGTCAAAAGGCAACAGAGTTCATTGATTATTCCATAGAACAGTCACACCATGCAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCACACCCTTGCAGACACACTTGACCATGAAAGGTTCCTCAATGAAATGTTCCTCATTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MetArgAlaPheLeuArgAsnGlnLysTyrGluAspMetHisAsnIleIleHisIleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlnIleArgLysLeuArgHisArgLeuSerAsnPheProArgLeuProGlyIleLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ArgSerGlnLysAlaThrGluPhelleAspTyrSerIleGluGlnSerHisHisAlaIle
                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BA PC COMPOSIMES DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/974,546
FILING DATE: 10-Oct-2001
CLASSIFICATION NUMBER: 09/097,199
FILING DATE: 1998-06-12
ATTORNEY/AGENT INFORMATION:
NAME: NARASHIMA, Richard A.
REFERENTICATION NUMBER: P-42,023
REFERENTICATION NUMBER: USC:018
TELEPHONE: (512) 474-7577
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 2087 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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Matches:
Conservative:
Mismatches:
Indels:
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SEQUENCE DESCRIPTION: SEQ ID NO: 83:
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694.00
100.00%
100.00%
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
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Best Local Similarity:
Query Match:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 GlnIleArgLysLeuArgHisArgLeuSerAsnPheProArgLeuProGlyIleLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 CAGATCAGAAAATTGAGGCACAGATTAAGTAACTTCCCAAGGCTACCAGGCATTCTAGCT
                                                               O'Hara, S. Mark
Ralph, David
Veltri, Robert
TITLE OF INVENTION: BLOMARKERS AND TARGETS FOR DIAGNOSIS,
PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
CORRESPONDENCE: 87
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/974,546
FILING DATE: 10-0Ct-2001
FILOR APPLICATION UNROWN
PRIOR APPLICATION NUMBER: 09/097,199
ATTORNEY/AGENT INFORMATION:
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135
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Nakashima, Richard A.
REGISTRATION NUMBER: P-42,023
REFERENCE/DOCKET NUMBER: UROC:018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 99..503
SEQUENCE DESCRIPTION: SEQ ID NO: 85:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
Sequence 85, Application US/09974546
Publication No. US20030050470A1
GENERAL INFORMATION:
APPLICANT: An, Gang
                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 2505 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [ELEFAX: (512) 474-7577
                                                                                                                                                                                                      STREET: P.O. Box 4433 CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
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694.00
100.00%
100.00%
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COMPUTER READABLE FORM:
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COUNTRY: USA
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1 (bases 1 to 690)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J., A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BU242169 690 bp mRNA linear EST 26-NOV-2002
603779592F1 CSEQCHN34 Gallus gallus cDNA clone ChEST725h23 5', mRNA
                                         AY439721 Armigeres
BQ592283 BO12698-0
BZ521554 BOKABBD66
CC091268 CSU-K33r.
CC7472302 AGENCOURT
CE464906 Ligr-NGBBD011
CC300810 COABESTH
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae,
Phasianinae, Gallus.
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                                                                                                                                                                                                                                                                                                                                  AL665968 ABM467342 ACB069753
                                                                                                                                                                                                                                                                                                                BU264381
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Department of Biomolecular Sciences
University of Manchester Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Gallus gallus"
/mol type="mRNA"
/strain="Compton Line 151"
                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Manchester, M60 1QD, UK
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BE015616
BE015598
AG110445
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CN135272
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CB069753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (chicken)
Gallus gallus
                     069. .1
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1399
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721
732
781
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Fax: 01612360409
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PO Box 88,
 sequence.
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MEDLINE
PUBMED
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
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-MODEL=frame+ p2n.model.-DEV=xlh
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-MODEL=frame+ p2n.model.-DEV=xlh
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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CB286029 CMD29 B11
BW577636 BW557636
BW587739 BW587739
BW591794 BW591794
BU412225 603155489
BU436282 603155489
CV511381 kc40h08.y
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                                                                                                                                           1 MRAFLRNQKYEDMHNIHIL......TLGLECCLLYLSKTIHPQII 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                         68479088
           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                    OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                  34239544 segs, 19032134700 residues
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Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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                                                 BW569427 Satou unpublished cDNA linear EST 31-AUG-2004 BW569427 Yutaka Satou unpublished cDNA library (cstb) Ciona Bavignyi cDNA clone cstb014408 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                       398 AAAAAAGGAAAAAGAAAAGCACCACCACAAACTGAGATGCTGCTATTTCTCACTAAATGC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ciona savignyi
Ciona savignyi
Bukaryota: Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 588)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    509 AAATITAGGTGAAATAAAGAACAGTATACACTGATAAAGCTGCAGAG------AAT 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlySerSerMetLysCysSerSerLeuSerSerGluAlaIleLeuPheThrLeuThrLeu 111
                                                                                                                                                                                                                                                                                                                                                                                                                                               52 ValPheArgLysLysGluLysValLysArgSerGlnLysAlaThrGluPheIleAspTyr 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerIleGluGlnSerHisHisAlaIleLeuThrProLeuGlnThrHisLeuThrMetLys 91
                                                                                                                                                                                                                                                                                                                                                        15 AsnilelleHisileLeuGlnIleArgLysLeuArgHisArgLeuSerAsnPheProArg 34
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569 GTCCCAGGACTCCTGTTGCCCACAGAGAAACAGGTATTTGCTCAGCACTATCACAGTG
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CBZ86029 606 bp mRNA linear EST 27-FEB-2003
CMD29 B11_90 UMNMPM3 Sus scrofa cDNA clone PPSUBLIB_15B11 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 SerMetLysCysSerSerLeuSerSerGluAlaIleLeuPheThrLeuThrLeuGlnLeu 113
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Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
I (basea I to 606)
Dvorak,C.M.T., Hyland,K.A., Zhang,Y., Fahrenkrug,S.C. and
Murtaugh,M.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 AlaProGluThrValLeuLeuProPheCysTyrLysValPhe------ArgLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 AGCAATTTGCACCACGCTATATTTGCAGGGATTCAGTCATTCTTTCCACTGAGTGGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322 AGAGAGCACTGTTGCTTGTGCAGCTGCTGATACTGCCTC------CAGCGGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 Ser-----HisHisAlaIleLeuThrProLeuGlnThrHisLeuThrMetLysGlySer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    588
37
21
21
25
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                                                                                     Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
141. 81-75-705-4095
Fax: 81-75-705-1113
Email: yutaka@ascidian.zool.kyoto-u.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                           /organism="Ciona savignyi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Satou,Y. and Satoh,N.
Spressed genes in Ciona savignyi
Unpublished (2004)
Contact: Yutaka Satou
                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
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Sus scrofa
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AUTHORS
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	GenCore version 5.1.6	26	17	
	Copyright (c) 1993 - 2005 Compugen Ltd.	28	71	_
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OM protein - pr	OM protein - protein search, using sw model	31	71	_
		32	71	_
Run on:	September 9, 2005, 12:23:48; Search time 58 Seconds	33	71	
	(without alignments)	34	11	_
	900.218 Million cell updates/sec	35	71	_
		36	71	_
Title:	US-09-974-546C-86	37	71	_
Perfect score:	694	38	70.5	-
Sequence:	1 MRAFLRNQKYEDMHNIHILTLGLECCLLYLSKTIHPQII 135	39	70.5	_
		40	70	-
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•		45	69.5	_

Adg81358 Human AFP
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Abb80604 Human sbg

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ALIGNMENTS

AAW30601 ADQ89904 AAB18292 ABB80604

2105692

Total number of hits satisfying chosen parameters:

Listing first 45 summaries

Post-processing: Minimum Match 0% Maximum Match 100%

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* A_Geneseq_16Dec04:*

Database

geneseqp2001s:*

9 5

Nucleic acid marker; biomarker; tumour; prostate cancer; bladder cancer; benign prostatic hyperplasia; BPH; breast cancer; human; immunodetection. Prostate disease marker UC Band #28 amino acid sequence RW; Veltri AAY59296 standard; peptide; 135 AA. 99WO-US013151. 98US-00097199 Ralph D, (first entry) WPI; 2000-116557/10. N-PSDB; AAZ87584. (UROC-) UROCOR INC. O'hara SM, 19-APR-2000 Homo sapiens. 11-JUN-1999; 12-JUN-1998; W09964631-A1 16-DEC-1999. AAY59296; An G, RESULT 1 **AA**Y59296

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:*

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Description	Aay59296 Prostate	Aay59295 Prostate	Aau02174 Biomarker	Aau02175 Biomarker	Aay59294 Cancer bi	Aau02173 Biomarker	Ads41968 Bacterial	Adn18681 Bacterial	Abb90843 Herbicida	Adn48099 Thermococ	Adf50279 Human PFM	Ado36741 Human PR-	Abb58124 Drosophil	Ads08184 Staphyloc	Abm69043 Photorhab	Abu42279 Protein e	Abg18410 Novel hum	Aab46398 H. pylori	Adm94292 Soybean E	Adf41696 Bacillus	Adm94288 Corn Ethy	Abg15498 Novel hum	Aau42328 Propionib	Abm38847 Propionib	Aam39676 Human pol
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Score	694	694	694	694	103	103	90	90	82.5	81	77.5	77.5	77.5	77	76.5	75	73	72	72	71.5	71.5	71.5	71	71	71
Result No.	1	7	m	4	S	ø	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

The invention provides nucleic acid markers of prostate, breast and bladder cancer. The markers are indicators of malignant transformation of prostate, breast and bladder tissues and are diagnostic of the potential for metastatic spread of malignant prostate tumours. The nucleic acid can also be used as targets for therapeutic intervention in prostate cancer, benign prostatic hyperplasia (BPH), bladder cancer or breast cancer. The markers may be used to design specific probes and primers, for the rapid analysis of prostate, bladder or breast biopsy samples. The probes and primers may also be used for in situ hybridization or in situ PCR detection and diagnosis. They may also be used to identify and isolate full length gene sequences form various DNA libraries. Antibodies against the polypeptide products of the markers can be used to treat prostate cancer, bladder cancer or breast cancer. The encoded proteins may be used

Novel RNA biomarkers for diagnosis, prognosis and management of prostate, breast and bladder cancer.

Example 5; Page 184-186; 191pp; English.

for

immunodetection methods for detecting or quantifying the cancers, and for clinical diagnosis of these cancers. The antibodies may also be used for radioimaging to quantify and localize the encoded proteins

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                                                                                                                                                                                                                                                                       RSQKATEPIDYSIEQSHHAILTPLQTHLTMKGSSMKCSSLSSEAILFTLTLQLTQTLGLE 120
                                                                                                                                                                                                                                                                                                           120
to detect antibodies. The proteins and antibodies can be used in immunodetection methods for detecting or quantifying the cancers, and for clinical diagnosis of these cancers. The antibodies may also be used for radioimaging to quantify and localize the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid marker; biomarker; tumour; prostate cancer; bladder cancer; benign prostatic hyperplasia; BPH; breast cancer; human; immunodetection
                                                                                                                                                                                                                       1 MRAFLRNQKYEDMHNIIHILQIRKLRHRLSNFPRLPGILAPETVLLPFCYKVFRKKEKVK
                                                                                                                                                                                                                                                                                          61 RSQKATEFIDYSIEQSHHAILTPLQTHLTWKGSSWKCSSLSSEAILPTLTLQLTQTLGLE
                                                                                                                                                                                                 1 MRAFLRNQKYEDMHNIIHILQIRKLRHRLSNFPRLPGILAPETVLLPFCYKVFRKKEKVK
                                                                                                                                                                 Gaps
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                                                                                                                          100.0%; Score 694; DB 3; Length 135; 100.0%; Pred. No. 6.9e-75; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prostate disease marker UC Band #28 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Page 182-183; 191pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    An G, O'hara SM, Ralph D, Veltri RW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY59295 standard; peptide; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US013151
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                                                                                                                                             Best Local Similarity 100.
Matches 135, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-116557/10.
N-PSDB; AAZ87583.
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                                                                                           Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                              Query Match
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                                                                                                                          1 MRAFLRNQKYEDMHNIIHILQIRKLRHRLSNFPRLPGILAPETVLLPFCYKVFRKKEKVK
                                                                                                                                                                        61 RSQKATEFIDYSIEQSHHAILTPLQTHLTMKGSSMKCSSLSSEAILFTLTLQLTQTLGLE
                                                                                                                                                                                            61 RSQKATEFIDYSIEQSHHAILTPLQTHLTMKGSSMKCSSLSSEAILFTLTLQLTQTLGLE
                                                                                                    1 MRAFLRNOKYEDMHNIIHILOIRKLRHRLSNFPRLPGILAPETVLLPFCYKVFRKKEKVK
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biomarker protein encoded by UC band 28 #2, used in diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prostate; breast; bladder; cancer; biomarker; probe; diagnostic;
benign prostatic hyperplasia; BPH; therapeutic; human.
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                                Length 135;
                                                                 Indels
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                               100.0%; Score 694; DB 3;
100.0%; Pred. No. 6.9e-75;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                      AAU02174 standard; protein; 135 AA.
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96US-0013611P.
96US-00692787.
                           Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 135; Conservative C
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Sequence 135 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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11-JAN-1996;
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Length 135;

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Query Match
Best Local Similarity 100.0
Matches 135; Conservative
 Sequence 135 AA;
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                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acids as biomarkers and targets useful for detecting, diagnosing, prognosing, and in developing treatments for prostate, breast and bladder cancer.
                                                                                                                                         61 RSQKATEFIDYSIEQSHHAILTPLQTHLTMKGSSMKCSSLSSEAILFTLTLQLTQTLGLE 120
                                                                                             9
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                                                                                                                                                                                                                                                                                                                                             Biomarker protein encoded by UC band 28 #3, used in diagnosis of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents the amino acid sequence of biomarker protein encoded by UC band 28 #3. Proteins encoded by the nucleic acid markers can be used to produce antibodies for the detection of prostate, breast or bladder cancer. Biomarker nucleic acid sequences can be used as
                                                                                                          1 MRAFLRNOKYEDMHNIIHILQIRKLRHRLSNFPRLPGILAPETVLLPFCYKVFRKKEKVK
                                                                                                                                                      61 RSQKATEFIDYSIEQSHHAILTPLQTHLTMKGSSMKCSSLSSEAILFTLTLQLTQTLGLE
                                                                                           1 MRAFLRNOKYEDMHNIIHILQIRKLRHRLSNFPRLPGILAPETVLLPFCYKVFRKKEKVK
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                   Prostate; breast, bladder; cancer; biomarker; probe; diagnostic;
benign prostatic hyperplasia; BPH; therapeutic; human.
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                                              Length 135;
                                                                    Indels
                                             100.0%; Score 694; DB 4;
100.0%; Pred. No. 6.9e-75;
ive 0; Mismatches 0;
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cancer cells in a biological sample
                                                                                                                                                                                                                                                                        AAU02175 standard; protein; 135 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Col 125; 78pp; English
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96US-0013611P.
96US-00692787.
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                                                        Best Local Similarity 100.
Matches 135; Conservative
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                        Sequence 135 AA;
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11-JAN-1996;
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                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the polypeptide products of the markers can be used to treat prostate cancer, bladder cancer or breast cancer. The encoded proteins may be used to detect antibodies. The proteins and antibodies can be used in immunodetection methods for detecting or quantifying the cancers, and for clinical diagnosis of these cancers. The antibodies may also be used for radioimaging to quantify and localize the encoded proteins
                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                             61 RSQKATEFIDYSIEQSHHAILTPLQTHLTMKGSSMKCSSLSSEAILFTLTLQLTQTLGLE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              benign prostatic hyperplasia; BPH; breast cancer; human; immunodetection.
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                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                     RSQKATEFIDYSIEQSHHAILTPLQTHLTMKGSSMKCSSLSSEAILFTLTLQLTQTLGLE
                                                                                                                                                      1 MRAFLRNOKYEDMHNITHILQIRKLRHRLSNFPRLPGILAPETVLLPFCYKVFRKKEKVK
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100.0%; Score 694; DB 4;
100.0%; Pred. No. 6.9e-75;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY59294 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCLLYLSKTIHPQII 135
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cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistence; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

bacterial polypeptide

US2003233675-A1.

Bacteria.

18-DEC-2003,

Recombinant DNA construct; transformed plant; improved plant property;

Bacterial polypeptide #20398.

02-DEC-2004 (first entry)

ADS41968;

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                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acids as biomarkers and targets useful for detecting, diagnosing, prognosing, and in developing treatments for prostate, breast and bladder cancer.
                             Gaps
                                                                                                                                                                        Biomarker UC band 28, antigenic peptide used in diagnosis of cancer.
                                                                                                                                                                                          Prostate; breast; bladder; cancer; biomarker; probe; diagnostic; benign prostatic hyperplasia; BPH; therapeutic; human; antigenic
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           Length 21;
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                            Indels
        14.8%; Score 103; DB 3; L. ilarity 100.0%; Pred. No. 5.7e-05; Conservative 0; Mismatches 0;
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Pred. No. 5.7e-05;
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100.0%; Pred. No. ...
0; Mismatches
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                                               54 RKKEKVKRSQKATEFIDYSIE 74
                                                         1 RKKEKVKRSQKATEFIDYSIE 21
                                                                                                                AAU02173 standard; peptide; 21 AA.
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96US-00692787.
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                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                          O'hara SM, Ralph
Query Match
Best Local Similarity
Lang 21; Conserve
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Best Local Similarity
Matches 21; Conserv
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Goldman BS;

Chen X,

Slater SC,

Hinkle GJ,

Cao Y,

GOLDMAN B S. HINKLE G J. SLATER S C.

CHEN X

(CHEN/) (HINK/) CAOY/)

WPI; 2004-061375/06.

20-FEB-2003; 2003US-00369493. 21-FEB-2002; 2002US-0360039P.

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypoptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant with the cacombinant DNA construct and growing the transformed plant with the polynucleotide or polypeptide is useful for improving plant with the polynucleotide or polypeptide is useful for improving plants with improved plant properties, e.g. improved cold, heat or accompliate.

The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or accomplication. Collerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the plant growth rate by modification of carbohydrate, introgen or content, improved plant growth and development under at least one stress condition, improved light production of photosynthesis or by production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence detail or this patent did not form part of the printed specification but was obtained in electronic form part of the printed specification but was obtained in electronic form part of the printed specification but was obtained in electronic form at from USPTO at seqdata.uspto.gov/sequence.thml.
New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 MHNIIHILQIRKLRHRL----SNFP------RLPGILAPETVLLPFCYKVF 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 8; Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.0%; Score 90; DB 8
26.8%; Pred. No. 0.1;
tive 23; Mismatches
                                                                                                                                                                                                              Claim 1; SEQ ID NO 20398; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 26.84
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 371 AA;
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ADS41968 ID ADS41968 standard; protein; 371 AA.

RESULT 7

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Gaps

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0; Indels

74 21

54 RKKEKVKRSQKATEFIDYSIE RKKEKVKRSOKATEFIDYSIE

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21; Conservative

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Sequence 645 AA;
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                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polymucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant the recombinant DNA construct and growing the transformed plant, where the combinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with cimproved plant properties, e.g. improved cold, heat or drought tolerance, compressed resistence to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                  54 RKKEKVKRSQKATEFI-DYSIEQSHHAILTPLQTHLTMKGSSM-KCSSLSSEAILFTLTL 111
           -----FLDV 70
                                                                                                                                                                                                                                                                           cold tolerance, heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                                    Recombinant DNA construct; transformed plant; improved plant property
Goldman BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 1334; 122pp; English
                                                                                                                                                                     ADN18681 standard; protein; 381 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Slater SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                          20-FEB-2003; 2003US-00369493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-FEB-2002; 2002US-0360039P
                                                                                                                                                                                                                                            polypeptide #1334.
                                                                                                                                                                                                                    (first entry)
                                                                                                  :1 | | |
130 KLWDTLG 136
                                                                                  112 QLTQTLG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAO Y.
HINKLE G J.
SLATER S C.
CHEN X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-061375/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GOLDMAN B S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hinkle GJ,
                                                                                                                                                                                                                                                                                                                                                                                          US2003233675-A1
                                                                                                                                                                                                                    02-DEC-2004
                                                                                                                                                                                            ADN18681;
                                                                                                                                                                                                                                                                                                                                                                  Bacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SLAT/)
(CHEN/)
(GOLD/)
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under at least one stress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 NLTYGLKSSEELNEFLKDFDIJHSHHA-FTPLSLKALKAGKNMEKGTLLTTHSISFAHES 132
phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----RLPGILAPETVLLPFCYKVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 MHNL--AIKLRERGHEVGIVTNNRPTGKEBELKRYGIELIKIPGIISP-----FLDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 RKKEKVKRSQKATEF1-DYSIEQSHHAILTPLQTHLTMKGSSM-KCSSLSSEAILFTLTL
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                      32;
                                                                                                                                                                                                                                                                                                                       DB 8; Length 381;
0.11;
                                                                                                                                                                                                                                                                                                                                                                                      38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; SEQ ID NO 54; 261pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herbicidally active polypeptide SEQ ID NO 54.
                                                                                                                                                                                                                                                                                                                                                                                      23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MHNI IHILQIRKLRHRL----SNFP----
                                                                                                                                                                                                                                                                                                                       Score 90;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB90843 standard; protein; 645 AA.
                                                                                                                                                                                                                                                                                                                       13.0%;
26.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-AUG-2001; 2001WO-EP009892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-AUG-2001; 2001WO-EP009892
                                                                                                                                                                                                                                                                                   Deery Match
Best Local Similarity 26.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weidler M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QLTQTLG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLWDTLG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-269010/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FARB ) BAYER AG.
                                                                                                                                                                                                                                                            Sequence 381 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200210210-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             herbicides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112
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54 RKKEKVKRSOKATEF-IDYSIBOSHHAILTPLOTHLTWKGSSM-KCSSLSSEAILFTLTL 111

21 MHQL--AIYLKKLGHDVSIVTNDLKTGKEKELEELGVGLVKVPGVISP-VLGINITY---

13 MHNIIHILQIRKLRHRLS--

--NFPRLPGILAPETVLLPFCYKVF 53

32;

Length 384; 42; Indels

11.7%; Score 81; DB 8; 23.3%; Pred. No. 1.3; ive 28; Mismatches 4;

Local Similarity 23.39 tes 31; Conservative

Matches

ftp.wipo.int/pub/published pct sequences

Sequence 384 AA;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Method for disrupting targeted gene in genome of organism particularly thermostable bacterium and with genome chips for analysis, applicable in studying gene structure and functions.
                                                                                                                                                                                                                                                                               gene disruption; gene targeting; marker gene; transformation; homologous recombination; hyperthermostable archaebacterium; KOD1; gene structure; gene function; enzyme activity; medicine; forensic science; food; drug inspection; molecular biology; immunology.
                                               -----LLPFCYKVFRKKEKVKRSQ
                                                                                     64 KATEFIDYSIEQSHHAILTPLQTHLTMKGSSMKC-SSLSSEAILFTLTLQLTQTLGLECC
                            Gaps
                            29;
         Length 645;
                                                                                                                                                                                                                                                            Thermococcus kodakaraensis KOD1 protein sequence SegID1977.
                            Indels
                           46;
         DB 5;
       ch 11.9%; Score 82.5; DE Similarity 23.5%; Pred. No. 1.7; 31; Conservative 26; Mismatches
                                              25 LRHRLSNF---PRLPGILAPETV------
                                                                                                                                                                                                                                                                                                                                                                                                                                 (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                ADN48099 standard; protein; 384 AA
                                                                                                                                                                                                                                                                                                                                                                                           29-AUG-2003; 2003WO-IB003597.
                                                                                                                                                                                                                                                                                                                                                                                                               30-AUG-2002; 2002JP-00319011
                                                                                                                                                                                                                                                                                                                                Thermococcus kodakaraensis
                                                                                                                                                                                                                                        (first entry)
                                                                                                                            123 LLYLSKTIHPQI 134
                                                                                                                                               212 AVWIPNEİKTEM 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Imanaka T, Atomi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-257583/24.
                                                                                                                                                                                                                                                                                                                                                   WO2004022736-A1
                                                                                                                                                                                                                                        01-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                       18-MAR-2004
       Query Match
Best Local Si
Matches 31
                                                                                                                                                                                                                     ADN48099;
                                                                                                                                                                                       ADN48095
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This invention relates to novel PFM (PR family member)/SET (Su(var)3-9, Enhancer-of-Zeete and Trithorax) nucleotides and encoded polypeptides thereof that are implicated in proliferative disorders such as cancer. Specifically, it refers to a functional fragment of the PFM/SET tumour suppressor gene that encodes a PR, SET, PRAZ or PKZL domain. The present invention describes the identification and characterisation of additional PR/SET-domain family members that can be used as regulators of cell proliferation and furthermore to treat, prevent or diagnose hyperproliferative disorders including scleroderma, arthritis, alcoholic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptides, useful for preventing or treating cancers, scleroderma, arthritis, keloids, atherosclerosis, Huntington's disease or Alzheimer's
                                                                                                                                                                                                                                                                                           Alzheimer's disease; paralysis; cerebellar atrophy; cytostatic; neuroprotective; nootropic; antiarthritic; vulnerary; antidiabetic; hepatotropic; PFM; PR family member.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New PR/SET-domain containing nucleic acids (which encodes PFM/SET) and
                                                                                                                                                                                         human, PPM7; SET; Su(var)3-9, Enhancer-of-Zeste and Trithorax; cancer; PPM/SET; tumour suppressor; hyperproliferative disorder; scleroderma; arthritis; alcoholic liver cirrhosis; hypertropic scarring; atthrosclerosis; gene therapy; buchenne's muscular dystrophy; insulin-dependent diabetes mellitus; Huntington's; Parkinson's;
                                                                                                                                                      Human PFM7 protein, a PR/SET family member.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 21; SEQ ID NO 4; 83pp; English.
                                      ADF50279 standard, protein, 1061 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JUL-2001; 2001US-00910478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUL-2001; 2001US-00910478
                                                                                                                12-FEB-2004 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-567062/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ADF50278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUAN/) HUANG S.
                                                                                                                                                                                                                                                                                                                                                                                                               US2003049623-A1
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-2003
                                                                           ADF50279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Huang S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease.
RESULT 11
                    ADF50279
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This invention relates to a novel method for targeting disruption of an arbitrary gene in a genome of an organism which comprises providing the whole sequential data of the genome of such organism, selecting at least a rabitrary region in the sequence, providing a vector that contains a sequence homologous with the selected region and a marker gene, transformation, and homologous recombination. The genome is preferably the genome of a hyperthermostable archaebacterium, particularly the genome of a hyperthermostable archaebacterium, particularly Thermococcus kodakazaensis KOD1. The method is for targeting the studying gene structure and functions as well as enzyme activities of encoded proteins and useful in medicine, forenaic science, food or drug inspection, molecular biology and immunology. With this method, the disruption of a gene at an arbitrary position in a genome can be achieved efficiently and reliably. The present sequence is that of a protein cencoded by the genome of Thermococcus kodakaraensis which was derived using the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at

Claim 9; SEQ ID NO 1977; 598pp; Japanese.

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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          704 HILKNHPGAELPPSIRKLRPAGPGEPDPMLSTHTQLTGTIATPPVCCPHCSKQYSSKTKM 763
liver cirrhosis, hypertropic scarring and atherosclerosis. Through gene therapy, these polynucleotides can be used to enhance proliferation of normal cells without rendering the cells cancerous and as such they are particularly useful for treating buchenne's muscular dystrophy, insulindependent diabetes mellitus, Huntington's, Parkinson's, Alzheimer's disease, paralysis, or cerebellar atrophy. Accordingly, these antiatthritic, vulnerary, antiatherosclerotic, neuroprotective, nootropic, antiathritic, vulnerary, antiatherosclerotic, antidiabetic or hepatocropic. This polypeptide sequence is the human PFM7 protein encoded by a PFM/SET gene localised to chromosome 11q25) of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 HILQ------IRKLR-----HRLSNFPRLPGILAPETVLLPPCYKVFRKKEKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 KR--SQKATEFIDYSIEQSHHAILTPLQTH-LTMKGSSMKCSSLSSEAILFTLTL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               31;
                                                                                                                                                                                                                                                                                                                                                                                            11.2%; Score 77.5; DB 7; Length 1061; 28.6%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 28.6*
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                        Sequence 1061 AA;
                                                                                                                                                                                                                                                                                    invention.
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764 VQHIRKKHPEFAQLS----NTIHTPLTTAVISATPAVLTTDSATGETVVTTDLTQAMT 818 112 QLTQTL 117 819 ELSQTL 824 ò 셤 ò g

ADO36741 standard; protein; 1061 AA ADO36741; RESULT 12 AD036741

Human PR-domain containing protein PFM-7. (first entry) 15-JUL-2004

cytostatic; histone methyltransferase; gene therapy; PFM/SET protein binding motif; cell growth modulator; histone methyltransferase activity; proliferative disorder; cancer; PR-domain; PFM-7.

US2004014192-A1 Homo sapiens

22-JAN-2004

18-JUL-2002; 2002US-00200012

18-JUL-2002; 2002US-00200012

(HUAN/) HUANG S

ŝ Huang WPI; 2004-121568/12.

New isolated nucleic acid molecule comprising a sequence encoding a PFM/SET polypeptide, useful for diagnosing, prognosing, preventing and treating proliferative disorders, e.g. cancer.

Claim 1; SEQ ID NO 4; 38pp; English.

The invention describes an isolated nucleic acid molecule comprising a sequence encoding a PFM/SET protein binding motifs polypeptides comprising a 689, 1061, 367, 717, 571, 951, 1257, 720, 720, or 770 amino acid sequence (P1-P9), given in the specification. Also described are: a vector comprising the isolated nucleic acid molecule; a host cell

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comprising the vector; an oligonucleotide comprising at least 17
contiguous nucleotides of the nucleic acid molecule; a primer pair for
detecting PFM/SET nucleic acid molecule, comprising two isolated
coligonucleotides; detecting PFM/SET nucleic acid molecule in a sample;
coligonucleotides; detecting PFM/SET nucleic acid molecule in a sample;
condulating cell growth by introducing the vector into a host cell, and
expressing the encoded PFM/SET polypeptide in a mamount effective to
modulate growth of the cell; isolating PFM/SET polypeptide by growing the
nost cell under conditions appropriate for the expression of the
polypeptide; the isolated PFM/SET polypeptide, or its functional fragment;
an isolated immunogenic PFM/SET polypeptide, comprising at least 8
contiguous anino acide of PLP9; an antibody or its antigno-binding
fragment that specifically binds to PFM/SET polypeptide; detecting
Contiguous anino acide of PLP9; an antibody or its antigno-binding
PFM/SET polypeptide in a sample; and screening for a compound that
conducting the polypeptide with one or more candidate compounds, and
determining histone methyltransferase activity of the contacted
colfiguration produced methyltransferase activity of the contacted
colfiguration produced methyltransferase and methods are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              704 HILKANIPGAELPPSIRKLRPAGPGEPDPMLSTHTQLTGTIATPPVCCPHCSKQYSSKTKM 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                818
                                                                                                                                                                                                                                                                                                                                                    useful for diagnosing, prognosing, preventing and treating proliferative disorders, e.g. cancer. This is the amino acid sequence of PR-domain containing polypeptide PFM-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 KR--SQKATEFIDYSIEQSHHAILTPLQTH-LTMKGSSMKCSSLSSEAILFTLTL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 VQHIRKKHPEFAQLS----NTIHTPLTTAVISATPAVLTTDSATGETVVTTDLLTQAMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----HRLSNFPRLPGILAPETVLLPFCYKVFRKKEKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 8; Length 1061;
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given in the specification. Also described are: a recombinant expression given in the specification. Also described are: a recombinant expression vector; a cell comprising a recombinant expression vector of (1); producing an S. epidermidis polypeptide; an isolated nucleic acid comprising a nucleotide sequence of at least 8 nucleotides in length; a vaccine composition for prevention or treatment of an S. epidermidis infection, comprising a nucleic acid cited above and a carrier; treating a subject for S. epidermidis infection; a recombinant or substantially pure preparation of an S. epidermidis polypeptide or its fragment; a vaccine composition for prevention or treatment of an S. epidermidis infection; detecting the presence of a Staphylococcus nucleic acid in sample; a computer readable medium having recorded in it the nucleotide sample; a computer readable medium having recorded in it the nucleotide sample; a computer based system for identifying fragments of the Staphylococcus genome of commercial importance; a computer based system for identifying commercially important nucleic acid fragments of the Staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphylococcus staphyloco
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                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                     Disclosure; SEQ ID NO 1164; 21pp + Sequence Listing; English.
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Matches 30; Conservative
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N-PSDB; ADS04412.
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RESULT 14 ADS0818

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                                                                                                                                                                                                                       53 FRKKEKVKR---SQKATEFIDYSIEQSHHAI-------LTPLQTHLTMKG
                                                           48; Gaps
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                                                                                                                                                                                                                                                                                                                                SSMKCSSLSSEA-----ILFTLTLQLTQTLGLECCLLYLSKTIHPQII 135
                                                                                                                                                                                                                                                                                                                                                                  11.1%; Score 77; DB 8; Length 1026; 20.6%; Pred. No. 15; tive 33; Mismatches 54; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Photorhabdus luminescens protein sequence #2140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABM69043 standard; protein; 322 AA.
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WPI; 2003-148459/14.

The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are proteins from Photorhabdus luminescens. The isolated sequences are cources of probles and primers for detecting the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the CD lypoptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing vector inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. CC luminescens. Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The combinant production of the proteins, particularly toxins and antibacterials vectors containing the genes and Ab are also useful ctherapeutically (to treat microbial infection by bacteria or fungithat are sensitive to P. luminescens encoded toxins or antibiotics) and as CC factors and for identifying targets of human diseases for which P. CC luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides. Claim 2; SEQ ID NO 2140; 1205pp; French

Sequence 322 AA;

Query Match
11.0%; Score 76.5; DB 6; Length 322;
Best Local Similarity 26.6%; Pred. No. 3.5;
Matches 29; Conservative 19; Mismatches 50; Indels 11; Gaps

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13 MHNIIHILQIRKLRHRLSNPPRLPGILAPETVLLPPCYKVFRKKBKVKRSQKATEFIDYS 72

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Copyright (c) 1993 - 2005 Compugen Ltd.
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-016 8283 -016 8284 -016 8285 -16 8285 -16 8285 -16 8285 -16 8285 -16 8285 -16 8285 -10 -27 -10 -27			DB 3; 4.7e-77; es 0;
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ของของของของของของของขอ จัดกับเท่ากันสัสสัสสัสสัสสัสษ์		PE 113ARAN : CALDON : OF THE STATEMENT O	ilarity Conser
000 00 40 000 00 44 0000 0000 0000 000 0		SULT 1 Sequence 84, Application US/09097 Patent No. 6218529 GENERAL INFORMATION: APPLICANT: An, Gang APPLICANT: O'Hara, S. Mark APPLICANT: Veltri, Robert TITLE OF INVENTION: BIOMARKER TITLE OF INVENTION: BIOMARKER TITLE OF INVENTION: PROGNOSIS NUMBER OF SEQUENCES: 87 CORRESPONDENCE ADDRESS: ADDRESSES: ARDOLG, White & STREET: P.O. Box 4433 CITY: HOUSTON STATE: P.O. Box 4433 CITY: HOUSTON STREET: P.O. Box 4433 CITY: HOUSTON STREET: P.O. Box 4433 CONFURRY: USA ZIP: 77210 COMPUTER READBAILE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIDLE OPERATION SYSTEM: DC-DOS/MS SOFTWARE: PREDICATION DATA: APPLICATION NUMBER: US/09/0 FILING DATE: J-UUL-1996 ATTORNEY/AGENT INFORMATION: REFERENCE/DOCKET NUMBER: UR TELECHOME: (512) 414-7577 INFORMATION FOR SEQ ID NO: 84: TELECHOMINICATION INFORMATION: TELECHOMINICATION: TELECHOMINICATION INFORMATION: TELECHOMINICATION: TELECHOMINICATION INFORMATION: Match Local Similarity 100 hes 135; Conservative	
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CLASSIFICATION:
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                                                                    US-09-949-016-9182
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                    1 MRAFLRNOKYEDMHNIIHILQIRKLRHRLSNFPRLPGILAPETVLLPFCYKVFRKKEKVK 60
MRAFLRNOKYEDMHNIIHILQIRKLRHRLSNFPRLPGILAPETVLLPFCYKVFRKKEKVK 60
                                                                                                                                                                           Sequence 86, Application US/09097199;
Sequence 86, Application US/09097199;
Patent No. 6218529
GENERAL INFORMATION:
APPLICANT: An, Gang
APPLICANT: Raibh, David
APPLICANT: Weltri, Robert
ITILE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
ITILE OF INVENTION: PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTY: USA
ZIP: ...
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COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,199
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Pred. No. 4.7e-77;
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0; Mismatches
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TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 135; Conservative
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MEDIUM TYPE: Floppy of
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US-09-097-199-86
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Sequence 86, Appl
Sequence 56, Appl
Sequence 20398, A
Sequence 322997,
Sequence 324106,
Sequence 324108,
Sequence 324095,
Sequence 148597,
Sequence 324095,
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1014.252 Million cell updates/sec
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1: (cgn2_6/ptodata/2/pubpaa/US07_PUBCCMB.pep:*

1: (cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

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GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
                                                                                                       Length 135;
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COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/09/974,546
FILING DATE: 10-Oct-2001
CLASSIFICATION: Unknown
                                                                                                                                                Indels
                                                                                                  100.0%; Score 694; DB 10;
100.0%; Pred. No. 9.1e-72;
ive 0; Mismatches 0;
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ADDRESSEE: Arnold, White & Durkee
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TELECOMMUNICATION INFORMATION:
         ; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-09-974-546-86
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RAPLICATION NUMBER: 09/097,199
FILING DATE: 1998-06-12
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Nakashima, Richard A. REGISTRATION NUMBER: P-42,023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 56, Application US/09974546 Publication No. US20030050470A1 GENERAL INFORMATION:
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STRANDEDNESS: <Unknown>
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O'Hara, S. Mark
Ralph, David
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INFORMATION FOR SEQ ID NO: 56
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                  121 CCLLYLSKTIHPQII 135
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                                                                                             Query Match
Best Local Similarity 100.0
Matches 135; Conservative
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Best Local Similarity 100.0
Matches 21; Conservative
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COUNTRY: USA
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APPLICANT: AD, GANG
APPLICANT: AD, GANG
RAIDH, DAVID
Voltri, Robert
TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                   1 MRAFLRNQKYEDMHNIIHILQIRKLRHRLSNFPRLPGILAPETVLLPFCYKVFRKKEKVK
                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                            Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/974,546

FILING DATE: 10-Oct-2001

CLASSIFTCATION: UNKnown

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 694; DB 10;
Best Local Similarity 100.0%; Pred. No. 9.1e-72;
Matches 135; Conservative 0; Mismatches 0;
REFERENCE/DOCKET NUMBER: UROC:018
TELEPHONE: (512) 418-3000
TELEPAX: (512) 418-7577
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 09/097,199
RILING DATE: 1998-06-12
ATTORNEY/AGENT INFORMATION:
NAME: Nakashima, Richard A.
RESISTRATION NUMBER: 9-42,023
REFERENCE/DOCKET NUMBER: UROC:018
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                     LENGTH: 135 amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: TYPE: Dinear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-09-974-546-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEG ID NO: 86:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-974-546-86
Sequence 86, Application US/09974546
Publication No. US20030050470A1
GENERAL INFORMATION:
APPLICANT: An, Gang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CCLLYLSKTIHPQII 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 CCLLYLSKTIHPOII 135
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STATE: Texas
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
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Gaps

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

September 9, 2005, 13:01:39 Run on:

9; Search time 14.5 Seconds (without alignments) 895.811 Million cell updates/sec

US-09-974-546C-86 694 1 MRAFLRNQKYEDWHNIHIL......TLGLECCLLYLSKTIHPQII 135 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

pIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	probable hexosyltr	hypothetical prote	$\overline{}$	hypothetical prote	Ē	X protein - human	hypothetical prote	hypothetical prote	ABC transporter (A	two-component sens	isoleucyl-trna syn	hypothetical prote	phosphoenolpyruvat	phosphoenolpyruvat	hypothetical prote	hypothetical prote	hypothetical prote	serine/threonine k	steroid 11beta-mon	1-phosphatidylinos	hypothetical prote	histidine-tRNA lig	glucose transporte	adapter protein CM	ryanodine receptor	hypothetical prote	ORF MSV224 probabl	probable secreted	adherence factor T
SUMMARIES	£	: ::	F86174	MNXRSA	T21328	D64555	A58456	A82069	T43782	B84040	D70045	T40751	T06761	A44831	AE2413	H71606	T27983	T00634	AC1917	S11338	S57085	C75006	H64203	A31986	T13151	S40450	B87682	T28385	A71609	D81702
	DB	! a	~	Н	N	N	~	N	N	~	N	N	~	Н	~	7	N	~	7	Н	7	~	Н	~	7	7	~	7	7	7
	* Query Match Length	381	645	495	3147	523	172	263	196	227	451	1064	404	982	982	1398	154	743	1850	503	2470	379	414	496	639			833	-	3225
•	A Query Match	13.0	11.9	11.5	11.3	11.2	10.7	10.7	10.4	10.3	10.3	10.2	10.1	10.1	10.1	10.0	9.9	6.6	9.0	6.6	9.9	9.8	9.8	9.8	9.8	9.8	7.6	9.7	9.7	9.7
	Score	06	82.5	80	78.5	78	74.5		72.5	71.5	71.5	70.5	70	70	2	69.5	69	69	69	68.5	68.5	68	68	68	68	68		67.5	67.5	67.5
	Result No.	1	7	m	4	ഗ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

RESULT 2

Pypothetical protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Dacession: R66174
R;Theologis, A.; Ecker, J. R.; Palm, C. J.; Federapiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hudhes, B.; Huizar, L. Nature 408, 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C. A;Authors: Hunter, Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

hypothetical prote	hypothetical prote	hypothetical prote	translation initia	protein kinase Dar	hypothetical prote	precorrin-2 C20-me	hypothetical prote	ethylene receptor	DNA mismatch repai	hypothetical prote	tuberous sclerosis	outer membrane pro	major outer membra	transcription fact	probable Fe-S oxid
T03757	E96506	B82440	T01452	A54099	837927	AC3341	T21716	T06537	H70327	T22376	A49420	D86597	H72027	A42029	F97147
7	Ŋ	7	7	~	0	7	~	7	N	~	7	7	~	N	~
126	213	317	347	517	587	244	447	635	859	908	1784	344	344	446	472
7.6	7.6	7.6	7.6	9.7	7.6	9.6	9.6	9.6	9.6	9.6	9.6	9.5	9.5	9.5	9.5
67	67	67	67	67	67	66.5	66.5	66.5	66.5	66.5	66.5	99	99	99	99
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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A; Reference number: JC1331
                                 A; Residues: 1-3147 <WIL>
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A; Residues: 1-172 <ZEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A58456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nonstructural protein NCVP2 - simian rotavirus SA11
NyAlternate names: nonstructural protein NS53
C; Species: simian rotavirus SA11
C; Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C; Accession: 808215
R; Mitchell, D.B.; Both, G.W.
Virology 174, 618-621, 1990
A; Title: Conservation of a potential metal binding motif despite extensive sequence dive A; Reference number: 808215; MUID: 90163231; PMID: 2154894
A; Accession: 808215
A; Molecule type: genemic RNA
A; Residues: 1-495
A; Cross-references: UNIPROT: P15687; EMBL: X14914; NID: 961889; PIDN: CAA33039.1; PID: 961896
C; Genetics:
A; Map position: segment 5
C; Superfamily: bovine rotavirus nonstructural protein NCVP2
C; Keywords: nonstructural protein; zinc finger
                                                                                                                                                                                   Cross-references: UNIPROT:P93825; GB:AE005172; NID:g2341041; PIDN:AAB70445.1; GSPDB:GN:Genetics:
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      99 MTHLLAGFTYGPHWPWVMTAVTVFKMLTGIVSFLTALSLVTLLPLLLKA--KVREFMLSK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 KATEFIDYSIEQSHHAILTPLOTHLTMKGSSMKC-SSLSSEAILFTLTLQLTQTLGLECC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 RCFLDNEP------HLLKLRTVKHPITK-DKLQCIIDLYNIIFPINDKVIRKFERMIK 121
                                                                                                                                                                                                                                                                                                                                                                                                               63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F25C8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T21328
R;Matthews, L.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19407
A;Recession: T21328
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                             -----LLPFCYKVFRKKEKVKRSQ
                                                                                                                                                                                                                                                                                                                                                            29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Gaps
                                                                                                                                                                                                                                                                                                             Length 645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 11.5%; Score 80; DB 1; Length 495; I Similarity 25.3%; Pred. No. 2.3; 24; Conservative 22; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                         46;
                                                                                                                                                                                                                                                                                                     Query Match
11.9%; Score 82.5; DB 2;
Best Local Similarity 23.5%; Pred. No. 1.7;
Matches 31; Conservative 26; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :| :|: |: | :| 12 QRKCRN--QYKIEWYNHLLLP----ITLNAAAFK 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 SQKATEFIDYSIEQSHHAILTPLQTHLTMKGSSMK 96
                                                                                                                                                                                                                                                                                                                                                                                                          25 LRHRLSNF---PRLPGILAPETV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 LLYLSKTIHPQI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 AVWIPNEİKTEM 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                              A;Residues: 1-645 <STO>
                                                                                                  A,Accession: F86174
A,Status: preliminary
A,Molecule type: DNA
                                                                                                                                                                                                                                                      Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Matches
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C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: D64555
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne,
Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N
A;Ritle: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Cross-references: UNIPROT:09XV66; EMBL:281512; PIDN:CAB04172.1; GSPDB:GN00023; CESP:F2E
A;Experimental source: clone F25C8
C;Genetics:
                                                                                                                                A,Gene: CESP:F25C8.3
Map position: 5
A;Introns: 32/2; 57/2; 73/3; 113/3; 157/3; 366/1; 456/1; 509/1; 638/1; 773/2; 848/1; 902/
/3; 2110/2; 2737/3; 2827/1; 2902/3; 3093/3; 3121/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F25C8.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; nucleic acid sequence not shown; translation not shown Molecule type: DNA A;Molecule type: DNA A;Residues: 1-523 <TOM>A;Residues: 1-523 <TOM>A;Cross-references: UNIPROT:025059; GB:AE000547; GB:AE000511; NID:g2313377; PIDN:AAD0735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and its expression i
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                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1571 RADKRNILLADNWQAKQQALRKSIHARQSTAVPRRESAMVGQPE-FASKAIKWMLMEKMQQ 1629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1630 BKEKEKEKEKEKEKEKEKEKEKOLKKQSVEQDHSSTDTEEDAQLPEKNKPML-----TYLRSLVLQ 1682
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C;Species: human hepatitis B virus
C;Date: 30-Sep-1993 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 KKEKVKRSQKATE--FIDYSIEQSHHAILTPLQTHLTMKGSSMKCSSLSSEAILFTLTLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 RAFLRN------QKYEDMHNIIHILQIRKLRHRLSNFPRLPGILAPETVLLPFCYKVFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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R;Zeng, M.; Huang, B.R.; Cai, L.W.; Pan, G.Z.
Chinese Biochem. J. 12, 22-26, 1996
A,Title: The sequence analysis of the hepatitis B virus (HBV) X gene
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 21;
                                                                                                                                                                                                                                                                                                                                                                    Length 3147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 523;
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                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                            Query Match
11.3%; Score 78.5; DE
Best Local Similarity 28.1%; Pred. No. 26;
Matches 41; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.2%; Score 78; DB 2
23.5%; Pred. No. 3.9;
tive 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1683 LVHSPISSVLKCCLL-LSVEQHKQMI 1707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 LTQ---TLGLECCLLYLSKTIHPQII 135
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Best Local Similarity 23.5%
Matches 24; Conservative
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OM protein - protein search, using sw model

September 9, 2005, 13:00:59; Search time 51.5 Seconds (without alignments) 1342.343 Million cell updates/sec Run on:

US-09-974-546C-86 694 1 MRAFLRNQKYEDMHNIHIL......TLGLECCLLYLSKTIHPQII 135 Title: Perfect score: Sequence:

1612378 seqs, 512079187 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

1612378

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q9qzy1 homo sapien	pyroc			Q99fx6 simian rota	Q99fx4 simian rota	P15687 simian 11 r		Q99fx7 simian rota	Q7jkt8 caenorhabdi	025059 helicobacte	Q86820 potato aucu	Q8tzu8 pyrococcus	Q9nxi4 homo sapien	Q863z2 homo sapien	homo	homo	drosc	Q9w3n0 drosophila		P41368 Btaphylococ	O7n442 photorhabdu	Q61rr8 photobacter	P61243 physcomitre	Q6gj08 staphylococ	Q6sif8 uncultured	Q6scj3 uncultured	Q7m022 hepatitis b	•		caenorhabd
SUMMAKIES	Q9GZY1	059512	P93825	Q7SZX8	Q99FX6	Q99FX4	VN53_ROTS1	Q99FX5	Q99FX7	Q7JKT8	025059	Q86820	Q8TZU8	Q9NXI4	086322	PRDA_HUMAN	Osuris	Q8T4E8	ONEM6O	VN53_ROTSP	SYIP_STAAU	Q7N442	Q6LRR8	YCF2_PHYPA	Q6GJ08	Q6SIF8	Q6SCJ3	Q7M022	Q9KP79	Q7 PNX8	99XX60
ength DB	135 2	381 2	645 2	451 2	414 2	479 2	495 1	496 2	496 2	3175 2	523 2	1646 2	358 2	931 2	1023 2	1061 1	1061 2	1117 2	1117 2	495 1	1024 1	321 2	398 2	2259 1	629 2	160 2	163 2	172 2	263 2	404 2	3184 2
% Query Match Length	100.0	13.0	11.9	11.7	11.5	11.5	11.5	11.5	11.5	11.3	11.2	11.2	11.2	11.2	11.2	11.2	11.2	11.2	11.2	11.1		11.0	11.0	11.0	10.8	10.7	10.7	10.7	10.7	10.7	10.7
Score	694	90	82.5	81	80	80	80	80	80	78.5	78	78	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77	77	76.5	76.5	76.5	75	74.5	74.5	74.5	74.5	74.5	74
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Q9FHK4	Q/R215	Q7P537	Q8RF89	021040	Q9TGM3	097034	Q9FT44	Q83DP2	QGRX30	Q6ALV1	Q8XLZ4	Q7RJY2	Q9K884
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10.6	9.07	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.3
73.5 10.6								72 10.4		72 10.4			71.5 10.3

ALIGNMENTS

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E E E	05-JUL-2004 UC28 protein Name=UC28:	(TrEMBLrel. ;	27, Lė	Last anno	tatio	annotation update)	te)				
888888	Homo sapiens (Human) Eukaryota, Metazoa, Mammalia, Eutheria, NCBI TaxID=9606;	(Human) tazoa; heria; 06;	Chordata; Primates;	Craniata; Vertebrata; Butel Catarrhini; Hominidae; Homo	a, Ve lini;	Vertebrata; ; Hominidae;	ta; E dae;	Euteleostomi; Homo.	ostomi	*	
RXCRE	SEQUENCE FROM N.A. TISSUE=Prostate cancer; MEDLINE=21028101; PubMe An G., Ng A.Y., Meka C.	E FROM N.A. Prostate cancer; s=21028101; PubMed=11156405 Ng A.Y., Meka C.S.R., Luo (=11156 .R., I	56405; Luo G.,	Bright	s.	., Caz	Cazares I	į. :		
RA RAT REL DR SO SO SO	Wright G.L. Jr., Veltri "Cloning and characteric prostate, breast, and b) Cancer Res. 60:7014-702 EMBL; AF189250; AG17111 GENEW, HGNC:21079; PBOVJ SEQUENCE 135 AA; 1572	Wright G.L. Jr., Veltri R.W., "Cloning and characterization prostate, breast, and bladder Cancer Res. 60:7014-7020(2000) EMBL, AR189257, AAG17118.1; Genew, HGNC:21079; PBOV1. SEQUENCE 135 AA; 15722 MW;	tri R.W.; erization d bladder 7020(2000) 7118.1; 7117.1; BOV1.	of car	28, a i."; B19837		gene	over6	overexpressed		i.
Query Best Match	Match Local Simi es 135;	100.0% Similarity 100.0% 5; Conservative	., ., 0	Score 6 Pred. N	ore 694; ed. No. 2. Mismatches	, DB 2; 2.9e-60; nes 0;	Length Indels	th 135, els	. 0	Gaps	,0
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<i>상</i> 원	61 RSQ1 	RSOKATEFIDYSIEQSHHAILTPLQTHLTMKGSSMKCSSLSSEAILFTLTLQLTQTLGLE 	SHHAII SHHAII	,TPLQTHI TPLQTHI	TMKGS	SMKCSS:	LSSEA LSSEA		1.01.70 	TLGLE TLGLE	120
දුරු	121 CCLI 	CCLLYLSKTIHPQII CCLLYLSKTIHPQII	135								
RESULT OS9512 ID OO DT OO DT OO OD OO	2 59512; 1-AUG-1998 1-AUG-1998 1-UJN-2003 Ypothetical	PRELIMINARY; (TrEMBLREL 07, (TrEMBLREL 24, (TrEMBLREL 24, PROFFER PH1844	4	PRT; Created) Last sequ Last anno	381 AA ence uj tation	'; 381 AA. sequence update) annotation update)	te)				

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 MHNL--AIKLRERGHEVGIVTNNRPTGKEBELKRYGIELIKIPGIISP------FLDV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 MHNIIHILQIRKLRHRL---SNFP-------RLPGILAPETVLLPFCYKVF 53
                                                                                                                                                          Kawarabayael Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Oteuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.;
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DNA Res. 5:55-76(1998).
EMBL, Apo00007; BAA30965.1; -.
PIR; F71196; F71196.
  Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Buehler E., Conway A.B., Conway A.R., Dewar K., Feng J., Ki
Kurtz D., Li Y., Shinn P., Sun H., Davis R.W., Ecker J.R.,
Federspiel N.A., Theologis A.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.0%; Score 90; DB 2; Length 381; 26.8%; Pred. No. 1.8; tive 23; Mismatches 38; Indels
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Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome; Hypothetical protein.
SEQUENCE 381 AA; 42826 MW; ED0EB0CAOCFSCAE1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
15-P19-25 protein (Putative ethylene receptor).
Name=F19F19.25; Synonyms=ERS2;
Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                   STRAIN=OT3;
MEDLINE=98344137; PubMed=9679194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 26.8
188 34; Conservative
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Submitted (AUG-1997)
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Submitted (AUG-1997)
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                                                 NCBI_TaxID=53953;
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64 KATEFIDYSIEQSHHAILTPLQTHLTMKGSSMKC-SSLSSEAILFTLTLQLTQTLGLECC 122
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                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Sakai H., Hua J., Chen Q.G., Chang C., Medrano L.J., Bleecker A.B.,

A Sakai H., Hua J., Chen Q.G., Chang C., Medrano L.J., Bleecker A.B.,

B. Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.

B. Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.

B. Shell, ARC4019015, AAC62209.1; -.

B. RHBL, ARC4019015, AAC62209.1; -.

B. PIR, F86174; F86174.

CO; GO:0004872; F:receptor activity, IEA.

CO; GO:000155; F:receptor activity, IEA.

CO; GO:000155; F:receptor activity, IEA.

CO; GO:000155; F:receptor activity, IEA.

CO; GO:000155; F:receptor activity, IEA.

CO; GO:000155; F:receptor activity, IEA.

CO; GO:000155; F:receptor activity, IEA.

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CO; GO:000155; F:receptor activity, IEA.

CO; GO:000155; F:receptor activity, IEA.

CO; GO:000155; F:receptor activity, IEA.

CO; GO:000155; F:receptor activity, IEA.

CO; GO:000487; F:receptor activity, IEA.

CO; GO:000487; F:receptor activity, IEA.

CO; GO:000487; F:receptor activity, IEA.

CO; GO:000487; F:receptor activity, IEA.

CO; GO:000487; F:receptor activity, IEA.

CO; GO:000487; Co:000487; II.

CO:000487; Co:000487; II.

CO:000487; Co:000487; II.

CO:000487; Co:000487; II.

CO:000487; Co:000487; II.
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Brachydanio rerio (Zebrafish) (Danio rerio).
Buachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2004 (TrEMBLrel. 26, Last annotation update)
SI:ZK13A21.9 (Novel protein similar to vertebrate microphthalmia-associated transcription factor (MTTF) and zebrafish transcription factor (MTTF) and zebrafish transcription
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Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
1- SINILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
EMBL; AL644847; CR530419.1; -.
HSSP; P22415; 1AN4.
InterPro: IRRO01092; HLH_basic.
Ffam; PF00010; HLH; 1.
SWART; SM00353; HLH; 1.
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                                                                                   SEQUENCE FROM N.A. Nourizadeh S., Chen Q.G., Bleecker A.B. Ecker J.R., Meyerowitz E.M.; Scher J.R., Meyerowitz E.M.; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 11.9%; Score 82.5; DB 2; Length 6 Local Similarity 23.5%; Pred. No. 17; es 31; Conservative 26; Mismatches 46; Indels
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
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